

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 06:25:17 ; Search time 6778 Seconds
(without alignments)
13028.785 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 aggggtcccttagccggggcgc.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	8					Description
	No.	Score	Match Length	DB	ID	
1	1180.4	50.9	1182	9	AY404343	AY404343 Homo sapi
2	912.2	39.3	2197	3	AK050128	AK050128 Mus muscu
3	857.4	37.0	1180	9	AY404344	AY404344 Pan trogl
4	853.2	36.8	879	5	BQ216829	BQ216829 AGENCOURT
5	754	32.5	759	7	CN396938	CN396938 170004177
6	738	31.8	916	6	CD050395	CD050395 AGENCOURT
7	733.8	31.6	1185	9	AY404345	AY404345 Mus muscu
8	731.6	31.5	1353	3	AK041045	AK041045 Mus muscu

	9	522.4	22.5	978	4	BI102968	BI102968	602888578
	10	506.4	21.8	510	7	CN396939	CN396939	170005999
	11	490.6	21.1	717	7	CR769328	CR769328	DKFZp4690
	12	488.6	21.1	761	4	BI559553	BI559553	603252894
c	13	463.6	20.0	694	2	AW173071	AW173071	xj82g11.x
c	14	457.6	19.7	659	6	CB435346	CB435346	615435 MA
	15	452.6	19.5	1723	3	AK052644	AK052644	Mus muscu
	16	452.2	19.5	771	7	CR767782	CR767782	DKFZp469C
	17	450	19.4	724	6	CB952493	CB952493	AGENCOURT
	18	444.4	19.2	481	6	CB158774	CB158774	K-EST0218
c	19	442	19.1	583	1	AI694348	AI694348	wd45g04.x
c	20	437.8	18.9	462	5	BX109306	BX109306	BX109306
c	21	435.8	18.8	439	1	AA633698	AA633698	ag87a11.s
	22	431.6	18.6	899	4	BI246549	BI246549	602958449
c	23	430	18.5	430	1	AI917116	AI917116	ts52a02.x
c	24	422	18.2	422	1	AI580389	AI580389	tm42f08.x
c	25	417	18.0	1055	1	AI654867	AI654867	wb65c12.x
	26	415.8	17.9	660	2	BB221592	BB221592	BB221592
c	27	410.2	17.7	478	1	AI015041	AI015041	ov51a05.s
	28	407.8	17.6	585	7	CR770709	CR770709	DKFZp469J
	29	406.4	17.5	901	4	BI827790	BI827790	603075472
	30	404.8	17.4	1021	7	CK231266	CK231266	ILLUMIGEN
c	31	400	17.2	543	2	AW236852	AW236852	xm49h11.x
	32	398.4	17.2	552	7	CV029784	CV029784	8702 Full
	33	396.4	17.1	721	4	BG972539	BG972539	602841125
c	34	393.4	17.0	470	1	AA974327	AA974327	oq10g06.s
	35	389	16.8	531	8	AQ386013	AQ386013	RPCI11-14
c	36	388.6	16.8	449	1	AI217703	AI217703	qh15e09.x
	37	387.8	16.7	738	6	CB954127	CB954127	AGENCOURT
	38	386.6	16.7	751	8	AQ748070	AQ748070	HS_5538_A
	39	384.8	16.6	886	4	BI101074	BI101074	602886333
c	40	384.6	16.6	454	1	AA970255	AA970255	op64h06.s
	41	384.4	16.6	751	6	CB952810	CB952810	AGENCOURT
	42	384.2	16.6	582	5	BP274546	BP274546	BP274546
	43	380.8	16.4	578	5	BP275078	BP275078	BP275078
c	44	380.4	16.4	580	6	CB423692	CB423692	597208 MA
c	45	376.8	16.2	566	6	CB433850	CB433850	610302 MA
	46	375	16.2	460	7	R19994	R19994	yg38h02.r1
	47	374.2	16.1	759	4	BG971626	BG971626	602840706
	48	372.4	16.1	565	4	BI538734	BI538734	434264 MA
	49	370.4	16.0	910	4	BI099853	BI099853	602884666
	50	368.4	15.9	763	6	CD241803	CD241803	AGENCOURT
	51	365.4	15.8	419	7	CR740722	CR740722	CR740722
c	52	364.6	15.7	619	9	CE584093	CE584093	tigr-gss-
	53	361.6	15.6	1193	4	BI102573	BI102573	602889579
c	54	357	15.4	363	7	Z39483	Z39483	HSC1BC022 n
	55	354.4	15.3	360	5	BP431975	BP431975	BP431975
c	56	346.8	14.9	357	1	AA747964	AA747964	nx79a08.s
	57	341	14.7	880	4	BI143297	BI143297	602907843
	58	339.2	14.6	1082	3	BC024453	BC024453	Mus muscu
c	59	336.2	14.5	363	2	BF510946	BF510946	UI-H-BI4-
	60	335	14.4	908	2	BF788011	BF788011	602113215
	61	334.4	14.4	342	5	BP431877	BP431877	BP431877
	62	331.8	14.3	349	7	F06529	F06529	HSC1BC021 n
	63	330.2	14.2	538	4	BG971731	BG971731	602838268
	64	329.6	14.2	776	4	BI220321	BI220321	602935611
	65	329	14.2	956	2	BF784727	BF784727	602111365

	66	323	13.9	785	2	BF780827	BF780827	602105713
c	67	317	13.7	706	9	CE140389	CE140389	tigr-gss-
	68	314.8	13.6	772	4	BI099719	BI099719	602884581
	69	314.6	13.6	769	2	AW044731	AW044731	um13h02.y
c	70	314.4	13.6	436	8	AQ476159	AQ476159	CITBI-E1-
	71	308.4	13.3	875	2	BF788790	BF788790	602107191
	72	305.6	13.2	786	6	CB953250	CB953250	AGENCOURT
	73	304.2	13.1	890	4	BI101705	BI101705	602887533
c	74	303	13.1	799	7	CK848020	CK848020	970722 MA
	75	301.2	13.0	777	4	BG972946	BG972946	602840675
	76	298.6	12.9	711	2	BF785562	BF785562	602112344
	77	298.6	12.9	965	2	BF789220	BF789220	602105115
	78	298.4	12.9	755	4	BI220886	BI220886	602937437
	79	296.4	12.8	878	2	BF782452	BF782452	602106160
c	80	296	12.8	455	2	AW380602	AW380602	RC2-HT027
	81	294.6	12.7	453	1	AA245657	AA245657	mx03a05.r
	82	293.4	12.6	459	5	BX951484	BX951484	DKFZp781F
	83	293	12.6	913	4	BG972966	BG972966	602840774
	84	292.2	12.6	1452	2	BF782437	BF782437	602106145
c	85	290.2	12.5	429	2	AW236558	AW236558	xm47g07.x
	86	288.6	12.4	776	2	BF781397	BF781397	602104580
	87	288.2	12.4	713	4	BI327590	BI327590	602979770
	88	286.4	12.3	555	5	BP332215	BP332215	BP332215
	89	284	12.2	551	2	BF785590	BF785590	602112377
	90	282.2	12.2	488	6	CB433209	CB433209	609534 MA
	91	277.8	12.0	788	2	BF781367	BF781367	602104549
	92	277.6	12.0	863	7	CF218052	CF218052	AGENCOURT
	93	275.6	11.9	699	2	AW319008	AW319008	un10f04.y
	94	275.2	11.9	735	4	BI332326	BI332326	602983510
	95	273.4	11.8	371	2	BE843851	BE843851	RC0-TN007
	96	273.2	11.8	696	2	BB653699	BB653699	BB653699
	97	271.8	11.7	766	6	CB600123	CB600123	AGENCOURT
	98	271	11.7	904	2	BF780781	BF780781	602103058
	99	270.4	11.7	654	2	AW318818	AW318818	un07h11.y
	100	268	11.6	695	2	BB598307	BB598307	BB598307
	101	267.8	11.5	1027	4	BG969791	BG969791	602838703
	102	267.4	11.5	668	2	BB660895	BB660895	BB660895
	103	266.6	11.5	758	4	BI332502	BI332502	602981312
	104	264.4	11.4	782	4	BG972529	BG972529	602841114
	105	261.8	11.3	602	6	CB601068	CB601068	AGENCOURT
	106	261.6	11.3	380	7	CR746104	CR746104	CR746104
	107	259.8	11.2	701	2	BF787378	BF787378	602113777
	108	258.8	11.2	812	4	BG969879	BG969879	602838824
	109	255.2	11.0	399	1	AA245658	AA245658	mx03a06.r
c	110	254.6	11.0	328	1	AI671780	AI671780	wa05h05.x
c	111	254.6	11.0	331	1	AI613123	AI613123	ty71h04.x
c	112	254.6	11.0	332	1	AI672388	AI672388	ty64f01.x
	113	254	10.9	916	2	BF687218	BF687218	602102243
c	114	253	10.9	923	5	BX694171	BX694171	BX694171
c	115	252.6	10.9	920	5	BX701766	BX701766	BX701766
c	116	251.4	10.8	922	5	BX701212	BX701212	BX701212
	117	247.8	10.7	647	2	BB637357	BB637357	BB637357
c	118	247.8	10.7	922	5	BX686029	BX686029	BX686029
	119	246.8	10.6	581	1	AI528034	AI528034	uj39b11.y
	120	246.8	10.6	593	1	AI526529	AI526529	uj39e10.y
c	121	246.6	10.6	345	2	AW779709	AW779709	hn84f05.x
	122	246.6	10.6	383	5	BX955526	BX955526	DKFZp781A

123	246.2	10.6	878	4	BG973007	BG973007	602841631
124	244.2	10.5	473	2	BF659710	BF659710	maa23c04.
c 125	243.8	10.5	919	5	BX698025	BX698025	BX698025
126	239.4	10.3	651	1	AI527981	AI527981	uj38e11.y
127	236.8	10.2	551	1	AI876961	AI876961	uj36h03.y
128	236.4	10.2	550	1	AI526647	AI526647	uj41b09.y
129	236	10.2	581	7	CF171593	CF171593	B0844F01-
130	235.4	10.1	726	6	CB600351	CB600351	AGENCOURT
131	233	10.0	534	1	AI787373	AI787373	uj31b07.y
c 132	231.2	10.0	891	5	BX687753	BX687753	BX687753
c 133	230.8	9.9	347	1	AI767712	AI767712	wh38h05.x
134	228.8	9.9	533	1	AI875380	AI875380	uk31e01.y
135	228.4	9.8	549	1	AI050425	AI050425	uc86b01.y
c 136	227.2	9.8	288	2	AW235540	AW235540	xn19d12.x
137	227.2	9.8	867	2	BF785547	BF785547	602112327
138	226.8	9.8	469	2	AW610950	AW610950	un74c08.y
139	225.2	9.7	531	4	BI463768	BI463768	603203473
c 140	225.2	9.7	891	5	BX699365	BX699365	BX699365
141	224.8	9.7	925	2	BF781667	BF781667	602104385
142	222.6	9.6	887	2	BF785369	BF785369	602111710
143	222.4	9.6	562	1	AI746748	AI746748	ul07a01.y
144	222.2	9.6	536	1	AI787361	AI787361	uj31a06.y
145	220	9.5	524	1	AI876741	AI876741	uj35c01.y
146	218.6	9.4	536	2	AW226792	AW226792	um62c04.y
147	217.8	9.4	638	4	BI100051	BI100051	602885109
148	217.6	9.4	517	5	BX512263	BX512263	BX512263
149	216.6	9.3	533	1	AI747909	AI747909	ul03h02.y
150	216.6	9.3	555	2	AW107039	AW107039	ul92b06.y
151	216.6	9.3	649	2	BF788330	BF788330	602114069
c 152	216.4	9.3	291	1	AI521956	AI521956	ti79e06.x
153	215	9.3	407	6	CB434861	CB434861	611551 MA
154	214	9.2	715	4	BG971579	BG971579	602840635
c 155	213.8	9.2	813	5	BX693887	BX693887	BX693887
156	213	9.2	546	2	AW475287	AW475287	un63h08.y
c 157	212.2	9.1	793	7	CF219588	CF219588	AGENCOURT
c 158	211.8	9.1	796	7	CF218053	CF218053	AGENCOURT
159	211.4	9.1	769	2	BF782853	BF782853	602107722
160	210.6	9.1	611	1	AL794601	AL794601	AL794601
161	208.8	9.0	515	2	BF532434	BF532434	602074477
162	208.4	9.0	1349	2	BF686940	BF686940	602102714
163	207.8	9.0	968	2	BF780880	BF780880	602105777
164	206.8	8.9	931	7	CF238676	CF238676	AGENCOURT
165	204.6	8.8	661	6	BY732658	BY732658	BY732658
166	202.4	8.7	489	5	BX522348	BX522348	BX522348
c 167	197	8.5	253	1	AI373521	AI373521	qz46f08.x
c 168	197	8.5	253	1	AI492912	AI492912	qz42f01.x
169	191.6	8.3	833	2	BF786313	BF786313	602112827
170	191.4	8.2	508	1	AL803540	AL803540	AL803540
c 171	191.4	8.2	721	4	BJ640903	BJ640903	BJ640903
172	187.6	8.1	958	2	BF782294	BF782294	602106080
173	187.2	8.1	488	2	AW105948	AW105948	um20c05.y
174	186.8	8.1	752	6	CB601161	CB601161	AGENCOURT
175	186	8.0	470	2	AW319385	AW319385	un15f02.y
176	184.6	8.0	1783	3	CR636858	CR636858	Tetraodon
c 177	183.2	7.9	361	1	AA730192	AA730192	nw41a02.s
178	183.2	7.9	375	1	AA715548	AA715548	nv53g11.r
179	183	7.9	758	4	BG969488	BG969488	602837021

180	179.8	7.8	478	1	AI874790	AI874790	ul28b05.y
181	179.4	7.7	389	5	BY105462	BY105462	BY105462
182	179	7.7	820	7	CF222788	CF222788	AGENCOURT
c 183	177.8	7.7	676	4	BJ641175	BJ641175	BJ641175
c 184	173.4	7.5	606	9	CE149561	CE149561	tigr-gss-
c 185	172.2	7.4	603	9	CE843398	CE843398	tigr-gss-
c 186	171.8	7.4	599	1	AA758115	AA758115	ah68d01.s
187	168.8	7.3	420	2	BB846612	BB846612	BB846612
188	168.8	7.3	831	7	CF219551	CF219551	AGENCOURT
c 189	168.4	7.3	673	1	AI746432	AI746432	ul07a01.x
190	168.2	7.2	443	1	AI182048	AI182048	ud73d07.y
191	167.4	7.2	209	7	CR746121	CR746121	CR746121
192	166.6	7.2	463	1	AI931234	AI931234	ul58e10.y
c 193	164	7.1	791	7	CF219552	CF219552	AGENCOURT
194	163.6	7.1	882	7	CF239400	CF239400	AGENCOURT
195	159.6	6.9	706	7	CN059643	CN059643	Salamande
c 196	159.2	6.9	301	1	AI891486	AI891486	ul59b08.x
197	158.6	6.8	896	6	CA973829	CA973829	AGENCOURT
198	158.4	6.8	542	4	BI218377	BI218377	602937760
199	158.4	6.8	594	8	AZ519016	AZ519016	RPCI-11-6
200	156.8	6.8	464	8	AQ199079	AQ199079	RPCI11-67
201	156.2	6.7	771	7	CF222154	CF222154	AGENCOURT
202	155.8	6.7	426	1	AI529289	AI529289	ui61f12.y
203	153	6.6	434	2	BB847184	BB847184	BB847184
204	152.4	6.6	428	2	BB847987	BB847987	BB847987
205	151.6	6.5	936	6	CA980884	CA980884	AGENCOURT
206	151.4	6.5	387	1	AA105944	AA105944	ml80g04.r
207	151	6.5	1946	3	AK050435	AK050435	Mus muscu
c 208	150	6.5	607	4	BJ631992	BJ631992	BJ631992
209	149.4	6.4	2573	3	AK004971	AK004971	Mus muscu
210	148.2	6.4	438	2	BB848332	BB848332	BB848332
211	147.8	6.4	1581	9	AY418358	AY418358	Mus muscu
212	147.6	6.4	426	2	BB847742	BB847742	BB847742
213	147.6	6.4	858	7	CN986339	CN986339	61948_125
c 214	147	6.3	651	5	BQ388289	BQ388289	NISC_mn28
215	146.4	6.3	827	7	CF219587	CF219587	AGENCOURT
216	146.2	6.3	426	2	BB846847	BB846847	BB846847
217	145.8	6.3	418	5	BY006680	BY006680	BY006680
218	145.6	6.3	838	5	BU899699	BU899699	AGENCOURT
219	144.8	6.2	424	2	BB848230	BB848230	BB848230
220	144.6	6.2	429	2	BB847232	BB847232	BB847232
221	144.2	6.2	493	1	AI746700	AI746700	ul06d06.y
c 222	144.2	6.2	644	4	BJ098498	BJ098498	BJ098498
223	143.6	6.2	437	1	AI891771	AI891771	ul59b08.y
c 224	143.4	6.2	1108	7	CO645645	CO645645	ILLUMIGEN
225	142	6.1	438	2	BB847387	BB847387	BB847387
226	141.4	6.1	430	1	AL778797	AL778797	AL778797
227	140.8	6.1	369	2	BB843421	BB843421	BB843421
228	140.6	6.1	933	7	CO775326	CO775326	ILLUMIGEN
229	140.2	6.0	1896	3	AK002736	AK002736	Mus muscu
230	138.8	6.0	418	2	BB847984	BB847984	BB847984
231	138.6	6.0	362	2	BB847614	BB847614	BB847614
232	138.6	6.0	370	2	BB843440	BB843440	BB843440
233	138.2	6.0	528	1	AI876859	AI876859	uj35a11.y
234	137.8	5.9	1892	3	AK034801	AK034801	Mus muscu
235	137.4	5.9	2575	3	BC048920	BC048920	Mus muscu
236	136	5.9	960	5	BQ713091	BQ713091	AGENCOURT

237	133.8	5.8	2895	3	AK083294	AK083294	Mus muscu
238	132.6	5.7	825	5	BP443785	BP443785	BP443785
239	132	5.7	1118	7	CK028589	CK028589	AGENCOURT
240	131.6	5.7	1642	6	CD013996	CD013996	90117309
241	131.4	5.7	927	5	BQ925596	BQ925596	AGENCOURT
242	130.8	5.6	1004	5	BQ942104	BQ942104	AGENCOURT
243	130.4	5.6	718	4	BJ038707	BJ038707	BJ038707
244	130.2	5.6	928	7	CK871071	CK871071	AGENCOURT
245	130	5.6	821	7	CK953540	CK953540	4093245 B
246	129.8	5.6	420	5	BY006031	BY006031	BY006031
247	129.8	5.6	432	2	BB846687	BB846687	BB846687
c 248	129.4	5.6	740	4	BJ640531	BJ640531	BJ640531
249	129.2	5.6	424	2	BB846725	BB846725	BB846725
250	129.2	5.6	599	4	BI387131	BI387131	BFL26_001
251	129.2	5.6	631	4	BI387132	BI387132	BFL26_001
252	129	5.6	818	2	BF687167	BF687167	602102982
253	128.2	5.5	1581	9	AY418356	AY418356	Homo sapi
254	127.4	5.5	425	2	BB844689	BB844689	BB844689
255	127.2	5.5	383	5	BY005749	BY005749	BY005749
256	127.2	5.5	415	2	BB847175	BB847175	BB847175
257	124.8	5.4	430	5	BY006688	BY006688	BY006688
258	124.8	5.4	1023	6	CD013994	CD013994	90130114
259	124.8	5.4	1336	6	CD013995	CD013995	90130122
260	124.6	5.4	735	7	CK949530	CK949530	4074896 B
261	124	5.3	1783	3	AK050327	AK050327	Mus muscu
262	123.6	5.3	338	2	BB846932	BB846932	BB846932
263	123	5.3	930	5	BQ934372	BQ934372	AGENCOURT
264	123	5.3	1957	3	CR671108	CR671108	Tetraodon
265	122.8	5.3	423	5	BY006690	BY006690	BY006690
266	122.6	5.3	825	5	BU240452	BU240452	603323679
267	122.4	5.3	830	6	CA493727	CA493727	AGENCOURT
268	122	5.3	977	7	CO579097	CO579097	ILLUMIGEN
c 269	121.6	5.2	527	8	AQ993185	AQ993185	RPCI-23-3
c 270	121.6	5.2	694	8	AZ085726	AZ085726	RPCI-23-6
271	121.6	5.2	810	7	CO574370	CO574370	AGENCOURT
272	121.6	5.2	843	7	CO558457	CO558457	AGENCOURT
c 273	121.2	5.2	567	4	BI443347	BI443347	dai90a05.
274	121	5.2	340	2	BB846937	BB846937	BB846937
c 275	120.8	5.2	405	1	AI433413	AI433413	ti65c03.x
276	120.8	5.2	2099	3	AK008601	AK008601	Mus muscu
277	120.4	5.2	596	1	AL781524	AL781524	AL781524
278	120.4	5.2	651	1	AA255327	AA255327	mz84f10.r
279	119.8	5.2	1130	3	CR646329	CR646329	Tetraodon
c 280	119.6	5.2	594	9	FR0049565	AL605374	Fugu rubr
281	119.2	5.1	737	7	CO562727	CO562727	AGENCOURT
282	119	5.1	795	5	BX880311	BX880311	BX880311
283	119	5.1	835	7	CO573273	CO573273	AGENCOURT
284	119	5.1	882	4	BI144244	BI144244	602907984
285	118.8	5.1	494	1	AI785732	AI785732	uj37h01.y
286	118.8	5.1	629	5	BP138260	BP138260	BP138260
c 287	118	5.1	148	2	BF089587	BF089587	CM2-HT094
288	117.6	5.1	2450	3	BC011409	BC011409	Homo sapi
289	117.4	5.1	768	5	BX876854	BX876854	BX876854
c 290	117.2	5.1	1067	9	CNS05HQH	AL337922	Tetraodon
291	116.6	5.0	738	6	CB418995	CB418995	591831 MA
292	115.4	5.0	619	9	FR0007657	Z91467	F.rubripes
293	115.4	5.0	962	4	BG969620	BG969620	602836951

294	115	5.0	615	1	AL803499	AL803499	AL803499
295	115	5.0	1030	5	BQ714919	BQ714919	AGENCOURT
296	114.4	4.9	704	6	CB518006	CB518006	ssalrgb53
297	114	4.9	2079	6	CD013998	CD013998	90117389
298	113.8	4.9	634	6	CB955397	CB955397	AGENCOURT
299	113.8	4.9	1005	4	BG167171	BG167171	602344696
300	113.4	4.9	618	1	AL787677	AL787677	AL787677
301	113.4	4.9	633	1	AL789572	AL789572	AL789572
302	113.4	4.9	759	4	BJ730921	BJ730921	BJ730921
303	113	4.9	677	7	CK981590	CK981590	4114067 B
304	113	4.9	1570	3	CR646752	CR646752	Tetraodon
305	112.8	4.9	685	4	BJ495916	BJ495916	BJ495916
306	112.4	4.8	774	7	CO423341	CO423341	GGEZHT100
307	111.6	4.8	513	2	BF105272	BF105272	601822259
308	111.4	4.8	606	6	CB581397	CB581397	AMGNNUC:C
309	111.4	4.8	2394	3	BC043491	BC043491	Homo sapi
c 310	111	4.8	1126	7	CO645680	CO645680	ILLUMIGEN
311	110.8	4.8	605	6	CB581581	CB581581	AMGNNUC:N
312	110.6	4.8	977	4	BI331895	BI331895	602982580
313	110.4	4.8	691	8	AZ614547	AZ614547	1M0443J19
314	110.4	4.8	1770	3	CR644097	CR644097	Tetraodon
315	109.4	4.7	510	6	CB286305	CB286305	CMD34_E11
316	109.2	4.7	410	2	AW226896	AW226896	um63b09.y
317	109.2	4.7	848	7	CN986271	CN986271	61879_125
318	108.4	4.7	867	7	CN172607	CN172607	AGENCOURT
319	107.8	4.6	514	6	CB286306	CB286306	CMD34_E12
320	107.4	4.6	673	6	CA042007	CA042007	ssalplnb5
321	107.2	4.6	685	5	BU136075	BU136075	603124201
322	107.2	4.6	839	7	CF249906	CF249906	esa006_a0
c 323	107.2	4.6	861	7	CN159685	CN159685	948778_MA
324	107.2	4.6	970	5	BU122351	BU122351	603146762
325	107.2	4.6	988	5	BU122681	BU122681	603149059
c 326	106.8	4.6	584	1	AL793872	AL793872	AL793872
c 327	106.2	4.6	840	4	BJ746350	BJ746350	BJ746350
328	106.2	4.6	888	9	AY418357	AY418357	Pan trogl
329	106	4.6	674	7	CK948396	CK948396	4073279 B
c 330	105.8	4.6	580	8	AQ059652	AQ059652	CIT-HSP-2
331	105.4	4.5	751	5	BP452350	BP452350	BP452350
332	104.8	4.5	700	6	CB497940	CB497940	omykrbhb0
333	104.6	4.5	383	2	AW107617	AW107617	ul93c02.y
334	104.6	4.5	653	6	CD309485	CD309485	StrPu691.
335	104.4	4.5	677	7	CK956169	CK956169	4096235 B
336	103.8	4.5	835	4	BI757311	BI757311	603029525
337	103.6	4.5	613	1	AL679732	AL679732	AL679732
338	103.4	4.5	652	6	CA343408	CA343408	673504 NC
c 339	102.8	4.4	1188	6	CD505366	CD505366	CDA73-C09
340	102.6	4.4	651	4	BJ094864	BJ094864	BJ094864
c 341	102	4.4	673	4	BJ640772	BJ640772	BJ640772
c 342	101.8	4.4	310	5	BX636608	BX636608	BX636608
343	101.8	4.4	701	1	AL133897	AL133897	DKFZp761K
344	101.6	4.4	492	4	BG970195	BG970195	602839368
345	101.6	4.4	2202	3	AK002629	AK002629	Mus muscu
346	101.4	4.4	781	1	AI529761	AI529761	ui82b06.y
347	101	4.4	652	4	BJ624350	BJ624350	BJ624350
348	101	4.4	879	7	CO774398	CO774398	ILLUMIGEN
349	101	4.4	1101	9	CNS059KU	AL327351	Tetraodon
350	100.8	4.3	315	1	AA104237	AA104237	mp01b01.r

351	100.8	4.3	588	5	BP448488	BP448488	BP448488
352	100.8	4.3	615	5	BP449052	BP449052	BP449052
353	100.8	4.3	794	4	BG575052	BG575052	602598159
354	100.8	4.3	913	7	CO579137	CO579137	ILLUMIGEN
355	100	4.3	974	7	CO579983	CO579983	ILLUMIGEN
356	100	4.3	996	5	BQ714776	BQ714776	AGENCOURT
357	99	4.3	617	4	BJ615347	BJ615347	BJ615347
358	98.6	4.2	708	4	BJ731220	BJ731220	BJ731220
359	98.6	4.2	708	7	CV527312	CV527312	CS_GIL_14
360	98.6	4.2	750	5	BP448650	BP448650	BP448650
361	98.6	4.2	1022	5	BM925650	BM925650	AGENCOURT
362	98.4	4.2	564	6	CA347839	CA347839	679020 NC
363	98.4	4.2	2306	3	BC012716	BC012716	Mus muscu
364	98.2	4.2	759	4	BI330877	BI330877	602981265
365	98.2	4.2	790	7	CO555662	CO555662	AGENCOURT
c 366	98.2	4.2	808	4	BJ716530	BJ716530	BJ716530
c 367	98	4.2	834	4	BJ746664	BJ746664	BJ746664
368	97.8	4.2	710	2	BB667498	BB667498	BB667498
c 369	97.6	4.2	761	1	AI118428	AI118428	ue40e09.x
370	97.4	4.2	656	5	BQ388290	BQ388290	NISC_mn28
371	97.4	4.2	728	6	CD493117	CD493117	CDA03-C12
372	97.4	4.2	807	5	BU901536	BU901536	AGENCOURT
373	97.4	4.2	921	7	CN065626	CN065626	D15_Ag2_p
374	97.2	4.2	697	2	BB667336	BB667336	BB667336
375	97.2	4.2	697	4	BG747143	BG747143	602704364
376	97	4.2	874	7	CN985398	CN985398	58371_126
377	96.6	4.2	581	1	AL791968	AL791968	AL791968
c 378	96.6	4.2	639	2	BF322562	BF322562	maa28e12.
379	96.4	4.2	654	4	BJ060547	BJ060547	BJ060547
c 380	96.4	4.2	861	7	CK974452	CK974452	4105352 B
381	96.4	4.2	871	5	BQ900474	BQ900474	AGENCOURT
382	96.4	4.2	913	5	BQ714368	BQ714368	AGENCOURT
383	96.4	4.2	938	5	BQ942682	BQ942682	AGENCOURT
384	96	4.1	643	7	CV222277	CV222277	Le_mx0_58
c 385	96	4.1	896	7	CN159120	CN159120	948155 MA
386	95.6	4.1	603	6	CB163625	CB163625	K-EST0224
387	95.6	4.1	662	1	AL792519	AL792519	AL792519
388	95.6	4.1	665	1	AL638480	AL638480	AL638480
389	95.4	4.1	573	1	AL789331	AL789331	AL789331
390	95.4	4.1	1131	2	BF687385	BF687385	602102551
391	95.2	4.1	611	7	CF250034	CF250034	esa007_f0
392	95.2	4.1	1005	2	BE870911	BE870911	601448862
393	95	4.1	430	2	BB847324	BB847324	BB847324
c 394	95	4.1	739	7	CO387359	CO387359	AGENCOURT
395	94.8	4.1	557	2	AW318536	AW318536	um98f10.y
396	94.6	4.1	573	7	CO298247	CO298247	EK172617.
c 397	94.6	4.1	598	1	AI303476	AI303476	ui71e01.x
c 398	94.4	4.1	555	1	AI265736	AI265736	uj05f12.x
399	94.4	4.1	934	2	BF786200	BF786200	602110490
400	94.2	4.1	415	1	AI959352	AI959352	fd08e07.y
401	94.2	4.1	561	7	CN227962	CN227962	RJB035D05
402	94.2	4.1	582	6	CA386855	CA386855	668573 NC
403	94.2	4.1	650	7	CV041502	CV041502	4139371 B
404	94.2	4.1	666	6	CA348546	CA348546	679900 NC
405	94.2	4.1	668	6	CA349227	CA349227	619554 NC
406	93.8	4.0	415	5	BY006441	BY006441	BY006441
407	93.8	4.0	424	2	BB844926	BB844926	BB844926

408	93.8	4.0	554	2	BE013295	BE013295	123199	MA
409	93.8	4.0	1192	2	BF789664	BF789664	602105279	
410	93.6	4.0	718	5	BX876842	BX876842	BX876842	
411	93.6	4.0	724	5	BX875102	BX875102	BX875102	
412	93.6	4.0	755	5	BX889578	BX889578	BX889578	
413	93.6	4.0	759	5	BX885634	BX885634	BX885634	
414	93	4.0	690	8	AZ614319	AZ614319	1M0443N05	
c 415	93	4.0	728	7	CN585956	CN585956	USDA-FP_1	
416	93	4.0	746	2	BF688309	BF688309	602185172	
c 417	93	4.0	822	7	CN761092	CN761092	ID0AAA2BE	
418	92.8	4.0	581	5	BP275541	BP275541	BP275541	
419	92.8	4.0	753	7	CK029964	CK029964	AGENCOURT	
420	92.8	4.0	777	7	CO573842	CO573842	AGENCOURT	
421	92.6	4.0	547	7	CR751755	CR751755	DKFZp469C	
c 422	92.6	4.0	774	7	CF343072	CF343072	AGENCOURT	
423	92.4	4.0	616	6	CB163341	CB163341	K-EST0224	
424	91.6	3.9	356	5	BY005600	BY005600	BY005600	
425	91.6	3.9	776	4	BI103442	BI103442	602888971	
426	91.2	3.9	572	2	AW917402	AW917402	EST348706	
427	91.2	3.9	722	6	CB951410	CB951410	AGENCOURT	
428	91	3.9	535	1	AL911920	AL911920	AL911920	
c 429	91	3.9	551	4	BJ021349	BJ021349	BJ021349	
430	91	3.9	606	4	BJ009417	BJ009417	BJ009417	
c 431	91	3.9	674	4	BJ020682	BJ020682	BJ020682	
c 432	91	3.9	687	4	BJ019313	BJ019313	BJ019313	
c 433	91	3.9	733	4	BJ516248	BJ516248	BJ516248	
c 434	91	3.9	753	4	BJ518554	BJ518554	BJ518554	
c 435	91	3.9	756	4	BJ533312	BJ533312	BJ533312	
436	90.8	3.9	667	7	CK947903	CK947903	4072727 B	
437	90.8	3.9	670	7	CN793669	CN793669	4128731 B	
438	90.8	3.9	732	7	CK967438	CK967438	4082607 B	
439	90.6	3.9	599	4	BJ493042	BJ493042	BJ493042	
440	90.6	3.9	616	4	BJ501742	BJ501742	BJ501742	
441	90.6	3.9	910	7	CN992653	CN992653	70709_125	
c 442	90.4	3.9	732	3	CNS08LE2	BX017142	Single re	
c 443	90.2	3.9	811	6	CD632277	CD632277	56066634J	
c 444	90	3.9	643	1	AI785430	AI785430	uj42b06.x	
c 445	90	3.9	725	4	BJ518275	BJ518275	BJ518275	
446	89.8	3.9	958	4	BG167110	BG167110	602344612	
c 447	89.8	3.9	1125	9	CNS03SJZ	AL258632	Tetraodon	
448	89.6	3.9	969	4	BG291839	BG291839	602386068	
449	89.4	3.9	904	5	BU121683	BU121683	603145755	
450	89.4	3.9	905	7	CN173591	CN173591	AGENCOURT	
c 451	89.2	3.8	674	7	CO704930	CO704930	DG32-292d	
c 452	89	3.8	127	2	BF514925	BF514925	UI-H-BW1-	
453	88.8	3.8	624	7	CN275923	CN275923	170004245	
454	88.8	3.8	975	2	BF533975	BF533975	602075137	
c 455	88.4	3.8	602	3	CNS08M60	BX018148	Single re	
456	88.2	3.8	398	5	BY006400	BY006400	BY006400	
c 457	88.2	3.8	823	2	BF689099	BF689099	602185172	
458	88.2	3.8	831	6	CD105882	CD105882	AGENCOURT	
459	88	3.8	812	4	BI221130	BI221130	602939634	
460	87.8	3.8	618	9	FR0007653	Z91463	F.rubripes	
461	87.8	3.8	891	4	BG189133	BG189133	RST8173 A	
462	87.4	3.8	510	5	BX483530	BX483530	DKFZp686C	
463	87.4	3.8	1201	9	CNS015XW	AL106046	Drosophil	
464	87.2	3.8	579	5	BP277054	BP277054	BP277054	

465	87	3.8	812	5	BU364284	BU364284	603584620
466	86.8	3.7	447	5	BX618498	BX618498	BX618498
c 467	86.8	3.7	615	7	CK133545	CK133545	RE29447.3
468	86.4	3.7	830	4	BG195984	BG195984	RST15067
469	86.2	3.7	550	1	AI097692	AI097692	ue35b11.y
c 470	86.2	3.7	658	6	CB503528	CB503528	ssalmge50
471	86	3.7	794	4	BI328333	BI328333	602985653
c 472	85.6	3.7	548	7	CO698361	CO698361	DG32-135b
c 473	85.4	3.7	618	9	FR0049525	AL605334	Fugu rubr
474	85.2	3.7	529	6	CB224174	CB224174	1JEJ32C4
475	85	3.7	1044	9	CNS044X4	AL274657	Tetraodon
c 476	84.8	3.7	659	7	CK132607	CK132607	RE03265.3
477	84.6	3.6	688	7	CK977467	CK977467	4108686 B
478	84.4	3.6	416	7	CF919654	CF919654	Bflor531.
479	84.4	3.6	455	4	BI387360	BI387360	BFL26_002
480	84.4	3.6	551	4	BI442788	BI442788	dai90a05.
481	84.4	3.6	702	5	BU038648	BU038648	DH02E04 H
482	84.2	3.6	581	5	BP360001	BP360001	BP360001
483	84.2	3.6	788	5	BX624452	BX624452	BX624452
484	84	3.6	303	7	CR738701	CR738701	CR738701
c 485	84	3.6	607	7	CK132585	CK132585	RE02574.3
486	83.8	3.6	428	5	BY006488	BY006488	BY006488
487	83.6	3.6	840	5	BX624575	BX624575	BX624575
c 488	83.2	3.6	708	5	BQ202033	BQ202033	UI-R-EB1-
489	83	3.6	660	6	CD703965	CD703965	EST20492
490	83	3.6	1068	5	BU145928	BU145928	AGENCOURT
491	82.6	3.6	728	4	BG569536	BG569536	602588811
492	82.4	3.6	736	7	CK950173	CK950173	4075687 B
493	82.2	3.5	625	7	CK951591	CK951591	4090903 B
494	82.2	3.5	1016	9	CNS03VYT	AL263054	Tetraodon
495	81.6	3.5	666	4	BG971005	BG971005	602840033
496	81.4	3.5	557	2	BF080461	BF080461	231360 MA
c 497	81.2	3.5	656	2	AW338024	AW338024	xw65c05.x
c 498	81.2	3.5	1080	9	CNS03FCV	AL241528	Tetraodon
499	81	3.5	551	6	CD331938	CD331938	StrPu537.
c 500	81	3.5	638	7	CK950104	CK950104	4075303 B
501	80.8	3.5	789	7	CO808016	CO808016	AGENCOURT
502	80.4	3.5	863	7	CK974673	CK974673	4105736 B
503	80.2	3.5	1100	5	BQ278891	BQ278891	AGENCOURT
504	79.6	3.4	578	7	CK888307	CK888307	SGP149514
505	79.4	3.4	696	4	BG971909	BG971909	602841666
506	79.4	3.4	886	4	BG402016	BG402016	602466734
507	79.2	3.4	651	7	CO259652	CO259652	4131159 B
508	79.2	3.4	842	7	CO246322	CO246322	AGENCOURT
c 509	79	3.4	514	1	AI132717	AI132717	ue33h09.x
510	79	3.4	707	7	CO641589	CO641589	USDA-FP_1
511	78.8	3.4	452	4	BM090021	BM090021	503910 MA
512	78.8	3.4	642	6	CB155303	CB155303	K-EST0213
513	78.8	3.4	759	7	CN275924	CN275924	170006008
514	78.6	3.4	328	5	BY005676	BY005676	BY005676
515	78.6	3.4	823	4	BG193837	BG193837	RST12973
516	78	3.4	801	4	BG212458	BG212458	RST32045
517	77.8	3.4	449	2	BF080415	BF080415	231292 MA
c 518	77.8	3.4	614	6	CB169862	CB169862	KSV603161
519	77.6	3.3	441	9	CNS07H5L	AL610635	Anopheles
c 520	77.6	3.3	589	1	AI256545	AI256545	ui87g04.x
c 521	77.6	3.3	592	7	CK131146	CK131146	GH06505.3

	522	77.2	3.3	425	4	BJ624661	BJ624661	BJ624661
	523	77	3.3	1297	3	AK078371	AK078371	Mus muscu
c	524	76.6	3.3	538	6	CD336301	CD336301	StrPu537.
c	525	76.6	3.3	616	4	BJ507779	BJ507779	BJ507779
	526	76.6	3.3	1107	5	BM924331	BM924331	AGENCOURT
	527	75.8	3.3	1118	2	BF582087	BF582087	602099271
	528	75.6	3.3	414	7	CO994585	CO994585	UMC-pd12
c	529	75.6	3.3	584	4	BJ023549	BJ023549	BJ023549
	530	75.6	3.3	652	4	BJ705583	BJ705583	BJ705583
	531	75.6	3.3	739	7	CO047895	CO047895	Lr_AT1CF
	532	75.4	3.2	935	4	BG427877	BG427877	602501564
	533	75.2	3.2	792	2	BF786091	BF786091	602110662
	534	75.2	3.2	1110	2	BF533824	BF533824	602075352
	535	75	3.2	568	1	AA212451	AA212451	mw76g12.r
	536	75	3.2	648	7	CN983881	CN983881	52591_126
c	537	75	3.2	732	4	BJ743004	BJ743004	BJ743004
	538	74.8	3.2	616	1	AA255225	AA255225	mz85d04.r
	539	74.6	3.2	494	4	BJ623942	BJ623942	BJ623942
	540	74.6	3.2	557	6	CB157680	CB157680	K-EST0216
	541	74.6	3.2	770	4	BG201991	BG201991	RST21337
	542	74.2	3.2	694	1	AU129743	AU129743	AU129743
	543	74.2	3.2	782	4	BG167429	BG167429	602342703
	544	74.2	3.2	812	1	AI663013	AI663013	uj69f10.y
c	545	74.2	3.2	915	3	CNS08R35	BX024525	Single re
	546	74	3.2	582	1	AA075453	AA075453	zm87e07.r
	547	73.8	3.2	778	7	CF250901	CF250901	esa018_e0
	548	73.6	3.2	136	1	AA073542	AA073542	mm94b03.r
	549	73.2	3.2	508	2	BF383473	BF383473	602045154
	550	73.2	3.2	599	4	BJ488432	BJ488432	BJ488432
	551	73.2	3.2	751	7	CR769273	CR769273	DKFZp469I
	552	73	3.1	533	2	BF131143	BF131143	601819955
	553	73	3.1	573	6	CB161428	CB161428	K-EST0221
	554	73	3.1	837	7	CN763566	CN763566	ID0AAA7BG
c	555	73	3.1	980	1	AI256260	AI256260	ui96h12.x
c	556	72.8	3.1	517	2	AW604423	AW604423	RC3-CT025
c	557	72.8	3.1	662	7	CK948186	CK948186	4072991 B
	558	72.8	3.1	723	4	BG424452	BG424452	602447772
c	559	72.6	3.1	565	7	CO328600	CO328600	EK291003.
	560	72.6	3.1	741	7	CR559577	CR559577	DKFZp459B
	561	72.4	3.1	584	6	CB586065	CB586065	AMGNNUC:N
	562	72.4	3.1	935	2	BF234991	BF234991	602027544
	563	72.2	3.1	765	7	CK959288	CK959288	4100123 B
c	564	72.2	3.1	781	4	BJ748442	BJ748442	BJ748442
	565	72	3.1	361	5	BY082449	BY082449	BY082449
	566	72	3.1	554	5	BP243787	BP243787	BP243787
	567	72	3.1	560	5	BX485008	BX485008	DKFZp686G
	568	72	3.1	670	7	CO641121	CO641121	USDA-FP_1
	569	72	3.1	775	4	BI144659	BI144659	602909950
	570	71.8	3.1	935	2	BF532873	BF532873	602074982
c	571	71.8	3.1	1028	9	CNS046W3	AL277212	Tetraodon
	572	71.6	3.1	729	5	BQ179273	BQ179273	UI-M-EW0-
	573	71.6	3.1	793	7	CF662633	CF662633	CcLL03a11
	574	71.4	3.1	690	6	CB467191	CB467191	732919 MA
c	575	71	3.1	430	4	BI451798	BI451798	TY14E03 h
	576	71	3.1	725	7	CK349802	CK349802	hggfha18B
	577	70.8	3.1	629	4	BM791817	BM791817	K-EST0071
c	578	70.6	3.0	512	1	AI265232	AI265232	ui97d02.x

579	70.4	3.0	680	5	BX889196	BX889196	BX889196
580	70.4	3.0	871	7	CN972726	CN972726	20223_124
581	70.4	3.0	944	9	CG770584	CG770584	TcB41.1_E
582	70	3.0	689	4	BM642521	BM642521	170006873
583	70	3.0	733	7	CO561098	CO561098	AGENCOURT
584	69.8	3.0	547	7	CR763995	CR763995	DKFZp469L
585	69.8	3.0	688	4	BG286763	BG286763	602382611
586	69.6	3.0	353	5	BY005597	BY005597	BY005597
c 587	69.6	3.0	484	1	AI265260	AI265260	ui97f08.x
588	69.6	3.0	698	7	CK450042	CK450042	893658 MA
589	69.4	3.0	563	4	BM624521	BM624521	170006874
590	69.4	3.0	722	5	BX879296	BX879296	BX879296
c 591	69.4	3.0	1199	6	CD503770	CD503770	CDA64-C01
592	69.2	3.0	789	7	CO558955	CO558955	AGENCOURT
c 593	69	3.0	315	5	BY356244	BY356244	BY356244
c 594	69	3.0	517	1	AI118387	AI118387	ue36a02.x
c 595	68.8	3.0	498	1	AI118135	AI118135	ue34c01.x
596	68.8	3.0	515	2	BB283598	BB283598	BB283598
c 597	68.8	3.0	669	4	BG203058	BG203058	RST22427
598	68.6	3.0	441	4	BG876589	BG876589	QV1-DT006
599	68.6	3.0	614	4	BM607789	BM607789	170006870
600	68.6	3.0	837	7	CN976403	CN976403	26464_125
601	68.6	3.0	847	4	BG400151	BG400151	602440934
602	68.6	3.0	855	7	CN977220	CN977220	27419_125
603	68.4	2.9	446	1	AL694265	AL694265	AL694265
604	68.2	2.9	428	8	AQ194654	AQ194654	RPCI11-48
c 605	68.2	2.9	480	1	AI787349	AI787349	uj66f05.x
c 606	68.2	2.9	666	7	CK838901	CK838901	UI-R-AC0-
607	68	2.9	445	7	CN750793	CN750793	ApDT-XXVI
608	68	2.9	510	1	AI386060	AI386060	mm15f04.y
609	67.8	2.9	512	6	CA380373	CA380373	659644 NC
610	67.8	2.9	563	7	CK349927	CK349927	hggfha20A
611	67.6	2.9	470	2	BB747310	BB747310	BB747310
c 612	67.6	2.9	672	6	CA331021	CA331021	hab31b10.
613	67.6	2.9	792	7	CO573111	CO573111	AGENCOURT
c 614	67.2	2.9	588	6	CB505187	CB505187	ssalmge50
615	67	2.9	400	7	CN976669	CN976669	26779_125
c 616	67	2.9	692	9	AG078157	AG078157	Pan trogl
617	67	2.9	738	7	CK474315	CK474315	AGENCOURT
c 618	66.6	2.9	535	7	CO284467	CO284467	EK166132.
619	66.6	2.9	616	2	AW701598	AW701598	uq88b10.y
620	66.6	2.9	631	4	BJ004103	BJ004103	BJ004103
621	66.6	2.9	742	6	CB952913	CB952913	AGENCOURT
622	66.6	2.9	821	6	CB200045	CB200045	AGENCOURT
623	66.4	2.9	571	1	AU243299	AU243299	AU243299
624	66.2	2.9	400	7	CO261693	CO261693	4134046 B
625	66	2.8	611	6	CA968819	CA968819	CcLL03a08
626	66	2.8	1447	7	CV200634	CV200634	km06e10.y
c 627	65.6	2.8	618	9	FR0007644	Z91454	F.rubripes
628	65.6	2.8	901	7	CN501635	CN501635	AGENCOURT
c 629	65.4	2.8	344	1	AJ283854	AJ283854	4A3B-AAG-
c 630	65.4	2.8	697	2	AW942728	AW942728	LD25345.3
631	65.4	2.8	805	5	BU124084	BU124084	603147892
632	65.4	2.8	829	2	BF782818	BF782818	602107680
633	65.2	2.8	632	4	BJ528642	BJ528642	BJ528642
634	65.2	2.8	762	1	AA717701	AA717701	vp94g02.r
635	65.2	2.8	903	7	CN157171	CN157171	945851 MA

c 636	65	2.8	572	7	CK604711	CK604711	UT01394.3
637	65	2.8	939	5	BQ922613	BQ922613	AGENCOURT
638	65	2.8	1109	6	CD505365	CD505365	CDA73-C09
639	64.8	2.8	196	1	AI317676	AI317676	uj22c05.y
640	64.8	2.8	458	7	CO265158	CO265158	EK141664.
641	64.8	2.8	650	6	CD596098	CD596098	RK100A2F1
642	64.8	2.8	713	6	CA347838	CA347838	679019 NC
c 643	64.8	2.8	815	1	AA986709	AA986709	uc80d04.x
644	64.6	2.8	759	4	BJ728374	BJ728374	BJ728374
645	64.4	2.8	492	1	AA493091	AA493091	vi71h01.r
646	64.4	2.8	647	1	AA880242	AA880242	vv98g03.r
647	64.2	2.8	854	4	BI147191	BI147191	602913291
648	64	2.8	463	1	AA895843	AA895843	vy34h02.r
649	64	2.8	469	6	CB147253	CB147253	K-EST0203
c 650	64	2.8	489	1	AA985955	AA985955	uc72h01.x
651	64	2.8	512	1	AL785003	AL785003	AL785003
c 652	64	2.8	547	7	CO696892	CO696892	DG32-1041
653	63.8	2.8	721	7	CK663177	CK663177	A296 Symb
654	63.8	2.8	891	4	BG426822	BG426822	602493003
655	63.8	2.8	966	2	BF027320	BF027320	601671692
c 656	63.6	2.7	705	6	CB165252	CB165252	ZDW602600
657	63.6	2.7	789	7	CN174688	CN174688	AGENCOURT
658	63.4	2.7	1716	6	CD013997	CD013997	90117357
659	63.2	2.7	364	5	BX872852	BX872852	BX872852
660	63.2	2.7	729	7	CO570100	CO570100	AGENCOURT
661	63.2	2.7	950	7	CO582747	CO582747	ILLUMIGEN
662	63	2.7	1267	4	BG210359	BG210359	RST29896
c 663	62.8	2.7	556	2	BE026512	BE026512	db27e05.x
664	62.8	2.7	731	7	CV434524	CV434524	CS_hyp_35
665	62.6	2.7	346	4	BM030341	BM030341	488958 MA
666	62.6	2.7	494	8	AQ620313	AQ620313	HS_5180_B
c 667	62.6	2.7	569	6	CA342060	CA342060	671852 NC
668	62.4	2.7	638	4	BM649075	BM649075	170006873
669	62.4	2.7	807	7	CK030429	CK030429	AGENCOURT
670	62.4	2.7	886	2	BF788242	BF788242	602113469
671	62.4	2.7	980	4	BG179775	BG179775	602328862
672	62	2.7	352	9	FR0049577	AL605386	Fugu rubr
673	62	2.7	605	9	FR0007158	Z90968	F.rubripes
c 674	62	2.7	624	4	BG302826	BG302826	fl39e03.x
675	62	2.7	952	5	BU122907	BU122907	603147125
676	61.8	2.7	630	6	CB577476	CB577476	AMGNNUC:U
c 677	61.8	2.7	631	7	CK132736	CK132736	RE07815.3
678	61.8	2.7	888	6	CD759765	CD759765	AGENCOURT
c 679	61.6	2.7	504	7	CO262072	CO262072	EK084327.
680	61.6	2.7	613	1	AA647358	AA647358	vp88c04.r
c 681	61.6	2.7	619	9	FR0007662	Z91472	F.rubripes
c 682	61.4	2.6	483	9	CL583901	CL583901	OB_Ba007
683	61.4	2.6	684	6	CD341703	CD341703	StrPu536.
684	61.4	2.6	852	6	CA976637	CA976637	AGENCOURT
685	61.2	2.6	368	5	BU473251	BU473251	603760179
c 686	61.2	2.6	596	9	FR0049628	AL605437	Fugu rubr
687	61.2	2.6	623	7	CK517693	CK517693	rswjb0_00
688	61	2.6	415	9	FR0014950	AL006159	F.rubripe
689	61	2.6	739	4	BG195983	BG195983	RST15066
690	61	2.6	1071	5	BU525573	BU525573	AGENCOURT
691	60.8	2.6	638	4	BI103514	BI103514	602889055
c 692	60.8	2.6	675	4	BJ136139	BJ136139	BJ136139

c 693	60.8	2.6	738	6	CB659466	CB659466	OSJNEc16H
694	60.8	2.6	806	1	AI048638	AI048638	ud64c07.y
c 695	60.8	2.6	829	6	CB666604	CB666604	OSJNEd13J
696	60.6	2.6	491	4	BG427032	BG427032	602493934
c 697	60.6	2.6	590	4	BJ142883	BJ142883	BJ142883
698	60.6	2.6	641	7	CF254125	CF254125	mdvn112_a
c 699	60.6	2.6	714	9	AG578491	AG578491	Mus muscu
c 700	60.6	2.6	728	4	BJ139199	BJ139199	BJ139199
c 701	60.6	2.6	732	7	CV516957	CV516957	0048P0018
702	60.4	2.6	312	9	FR0015816	AL007022	F.rubripe
703	60.4	2.6	581	1	AA473690	AA473690	vg89c08.r
c 704	60.4	2.6	638	7	CK940315	CK940315	4113683 B
c 705	60.4	2.6	638	7	CK955845	CK955845	4095851 B
c 706	60.2	2.6	811	8	BZ267251	BZ267251	CH230-262
707	60	2.6	495	1	AA674349	AA674349	vp98h05.r
708	60	2.6	784	9	CL311817	CL311817	286867_LB
709	59.8	2.6	497	1	AJ683303	AJ683303	AJ683303
710	59.8	2.6	546	1	AA575452	AA575452	vl90b05.r
711	59.8	2.6	552	1	AI286386	AI286386	ui75g08.y
712	59.8	2.6	728	7	CO641072	CO641072	USDA-FP_1
713	59.6	2.6	379	1	AV683166	AV683166	AV683166
714	59.6	2.6	399	7	T62130	T62130	yc66e11.rl
715	59.6	2.6	997	9	CNS005TE	AL060767	Drosophil
c 716	59.4	2.6	605	7	CK604610	CK604610	UT01321.3
c 717	59.4	2.6	650	9	CL196913	CL196913	104_423_1
718	59.4	2.6	681	7	CN790431	CN790431	4125029_B
c 719	59.4	2.6	815	9	CG231386	CG231386	OGWGN83TH
c 720	59.4	2.6	835	9	CG281350	CG281350	OGYAI36TV
721	59	2.5	634	4	BG642104	BG642104	pg11c.pk0
c 722	59	2.5	643	7	CK977010	CK977010	4108302 B
c 723	59	2.5	699	8	AZ947666	AZ947666	2M0210N24
c 724	59	2.5	717	4	BJ147817	BJ147817	BJ147817
725	59	2.5	853	2	BF232793	BF232793	602023393
726	59	2.5	952	2	BF232705	BF232705	602023293
727	58.8	2.5	522	7	CR771627	CR771627	DKFZp469F
728	58.8	2.5	542	4	BJ520742	BJ520742	BJ520742
c 729	58.6	2.5	82	1	AA974589	AA974589	op28h10.s
c 730	58.6	2.5	481	1	AI668249	AI668249	605018G07
731	58.6	2.5	484	5	BQ666537	BQ666537	pb43b12.y
c 732	58.6	2.5	493	1	AI664846	AI664846	605002D07
c 733	58.6	2.5	522	1	AI759125	AI759125	605085D09
c 734	58.6	2.5	528	6	CA401029	CA401029	EL01N0413
c 735	58.6	2.5	569	6	CA399837	CA399837	EL01N0326
c 736	58.6	2.5	572	6	CA404541	CA404541	EL01N0519
737	58.6	2.5	618	2	AW065890	AW065890	687002E04
c 738	58.6	2.5	621	9	CG303576	CG303576	OG0BG09TH
c 739	58.6	2.5	630	6	CA404340	CA404340	EL01N0515
c 740	58.6	2.5	656	6	CD446879	CD446879	EL01T0208
c 741	58.6	2.5	667	6	CA403669	CA403669	EL01N0505
c 742	58.6	2.5	683	4	BJ816482	BJ816482	BJ816482
743	58.6	2.5	685	9	CG296824	CG296824	OGWKC02TV
c 744	58.6	2.5	720	6	CA399209	CA399209	EL01N0315
c 745	58.6	2.5	720	6	CA401228	CA401228	EL01N0416
c 746	58.6	2.5	731	6	CA403005	CA403005	EL01N0445
c 747	58.6	2.5	749	3	AY112099	AY112099	Zea mays
c 748	58.6	2.5	758	6	CB653386	CB653386	OSJNEc04F
c 749	58.6	2.5	769	6	CD446561	CD446561	EL01T0203

c 750	58.6	2.5	785	6	CD446551	CD446551	EL01T0203
c 751	58.6	2.5	787	8	BZ637786	BZ637786	OGCBL09TM
c 752	58.6	2.5	799	9	CC724533	CC724533	OGWIZ79TV
c 753	58.6	2.5	820	6	CD437268	CD437268	EL01N0371
754	58.6	2.5	829	9	CG083392	CG083392	PUILH08TD
c 755	58.6	2.5	876	6	CD441044	CD441044	EL01N0551
756	58.4	2.5	942	7	CN990976	CN990976	67253_125
c 757	58.2	2.5	704	1	AU213104	AU213104	AU213104
758	58.2	2.5	1465	6	CD013999	CD013999	90117633
759	58	2.5	523	1	AA511527	AA511527	vj28d05.r
760	58	2.5	566	5	BP221553	BP221553	BP221553
c 761	58	2.5	842	7	CO161727	CO161727	FLD1_30_F
c 762	58	2.5	851	7	CO161650	CO161650	FLD1_30_F
c 763	57.8	2.5	461	1	AI256492	AI256492	ui87a02.x
c 764	57.6	2.5	355	9	CC465888	CC465888	ZMMBBc039
765	57.6	2.5	391	4	BG186196	BG186196	RST5044_A
c 766	57.6	2.5	578	9	CG301141	CG301141	OGXCC14TH
767	57.6	2.5	686	6	CD444925	CD444925	EL01N0445
768	57.6	2.5	823	4	BI332351	BI332351	602983540
769	57.4	2.5	628	1	AV657530	AV657530	AV657530
c 770	57.2	2.5	346	8	BZ348795	BZ348795	hp61d04.g
c 771	57.2	2.5	538	1	AL915629	AL915629	AL915629
772	57.2	2.5	558	1	AU201532	AU201532	AU201532
773	57.2	2.5	624	2	BE238993	BE238993	MD0649_Me
774	57.2	2.5	629	7	CK498980	CK498980	rswbb0_00
775	57	2.5	437	7	CF919695	CF919695	Bflor531.
c 776	57	2.5	447	6	CD441431	CD441431	EL01N0556
c 777	57	2.5	700	4	BJ148891	BJ148891	BJ148891
778	57	2.5	1101	9	CNS00KFD	AL077908	Drosophil
779	56.8	2.4	440	2	BB745467	BB745467	BB745467
780	56.8	2.4	445	7	CN955753	CN955753	3252_104-
781	56.8	2.4	601	7	CO637012	CO637012	USDA-FP_1
782	56.8	2.4	674	8	BZ328006	BZ328006	id33g10.g
c 783	56.8	2.4	807	8	BZ220205	BZ220205	CH230-360
784	56.8	2.4	837	9	CC659620	CC659620	OGXAA96TV
c 785	56.8	2.4	880	9	CC616166	CC616166	OGLCB41TH
786	56.8	2.4	1024	3	AY107409	AY107409	Zea mays
c 787	56.6	2.4	583	1	AI876537	AI876537	uj59f11.x
788	56.6	2.4	624	8	CC386454	CC386454	PUHPE49TD
c 789	56.6	2.4	628	8	CC386449	CC386449	PUHPE49TB
790	56.6	2.4	872	7	CN582253	CN582253	USDA-FP_1
791	56.4	2.4	632	6	CD748367	CD748367	rw36d05.y
c 792	56.4	2.4	732	4	BJ816728	BJ816728	BJ816728
c 793	56.4	2.4	743	4	BJ816263	BJ816263	BJ816263
c 794	56.4	2.4	749	4	BJ152595	BJ152595	BJ152595
c 795	56.4	2.4	768	4	BJ779102	BJ779102	BJ779102
c 796	56.4	2.4	775	4	BJ149607	BJ149607	BJ149607
c 797	56.4	2.4	777	4	BJ129204	BJ129204	BJ129204
798	56.4	2.4	814	4	BG428781	BG428781	602500860
c 799	56.2	2.4	426	7	CO308066	CO308066	EK256548.
c 800	56.2	2.4	629	6	CB494209	CB494209	omykrbhb0
c 801	56.2	2.4	793	4	BJ149397	BJ149397	BJ149397
802	56.2	2.4	809	4	BG971667	BG971667	602840766
803	56.2	2.4	1101	9	CNS000WU	AL053681	Drosophil
804	56	2.4	436	7	CO316063	CO316063	EK263564.
805	56	2.4	488	3	AY432118	AY432118	Aedes aeg
c 806	56	2.4	504	9	CG801172	CG801172	1118018D0

807	56	2.4	568	5	BP213630	BP213630	BP213630
c 808	56	2.4	695	4	BJ776790	BJ776790	BJ776790
c 809	56	2.4	785	9	CC659613	CC659613	OGXAA96TH
810	56	2.4	900	5	BU123073	BU123073	603149488
811	55.8	2.4	221	2	BB561857	BB561857	BB561857
812	55.8	2.4	316	7	CK942201	CK942201	4065834 B
c 813	55.8	2.4	619	9	FR0015790	AL006996	F.rubripe
c 814	55.8	2.4	704	1	AI529566	AI529566	ui82b06.x
815	55.8	2.4	1012	9	CNS0050V	AL056586	Drosophil
816	55.8	2.4	1266	9	CL962544	CL962544	OsIFCC007
817	55.6	2.4	353	2	AW424655	AW424655	707020H03
c 818	55.6	2.4	454	4	BJ817721	BJ817721	BJ817721
819	55.6	2.4	521	4	BM130311	BM130311	pb29d12.y
820	55.6	2.4	525	2	BE138067	BE138067	ug48a07.y
821	55.6	2.4	583	5	BX765624	BX765624	BX765624
822	55.6	2.4	633	5	BQ588578	BQ588578	E012562-0
c 823	55.6	2.4	716	1	AU216588	AU216588	AU216588
824	55.6	2.4	753	4	BI143423	BI143423	602907790
825	55.6	2.4	813	6	CA480775	CA480775	AGENCOURT
826	55.6	2.4	984	9	CNS006LF	AL065715	Drosophil
827	55.6	2.4	1009	9	CNS007PY	AL067477	Drosophil
c 828	55.4	2.4	309	9	CL583240	CL583240	OB_Ba004
829	55.4	2.4	548	7	CK886207	CK886207	SGP166618
c 830	55.4	2.4	675	4	BG320141	BG320141	Zm03_05c0
c 831	55.2	2.4	592	7	CO184970	CO184970	EC29003.3
832	55.2	2.4	713	7	CO638381	CO638381	USDA-FP_1
833	55.2	2.4	845	6	CA481394	CA481394	AGENCOURT
834	54.8	2.4	507	6	CB164110	CB164110	K-EST0225
835	54.8	2.4	570	5	BP257713	BP257713	BP257713
c 836	54.8	2.4	573	9	FR0049536	AL605345	Fugu rubr
c 837	54.8	2.4	619	9	FR0015778	AL006985	F.rubripe
c 838	54.8	2.4	734	4	BJ794516	BJ794516	BJ794516
839	54.6	2.4	584	1	AI987137	AI987137	rs22b08.y
840	54.6	2.4	603	5	BX499005	BX499005	DKFZp779A
841	54.6	2.4	619	6	CA100959	CA100959	SCCCFL100
842	54.6	2.4	644	5	BQ578506	BQ578506	WHE0304_F
843	54.6	2.4	739	4	BG969762	BG969762	602837258
844	54.4	2.3	464	6	CB953456	CB953456	AGENCOURT
845	54.4	2.3	542	8	BH778649	BH778649	fzmb013f0
c 846	54.4	2.3	604	5	BU050966	BU050966	1111036G0
847	54.4	2.3	661	7	CF623828	CF623828	zmrws05_0
848	54.4	2.3	662	7	CK827797	CK827797	zmrws05_0
849	54.4	2.3	737	9	CG370415	CG370415	OGWIZ79TH
850	54.2	2.3	372	1	AA675719	AA675719	MBAFCW4A0
c 851	54.2	2.3	574	4	BJ538530	BJ538530	BJ538530
852	54.2	2.3	576	4	BJ525957	BJ525957	BJ525957
853	54.2	2.3	628	2	BF787599	BF787599	602114528
854	54.2	2.3	1194	7	CV186196	CV186196	A-013 D.
855	54	2.3	427	7	CO285751	CO285751	EK060617.
856	54	2.3	463	6	CD915387	CD915387	G550.125P
857	54	2.3	580	5	BP215685	BP215685	BP215685
c 858	54	2.3	916	7	CV280250	CV280250	WS0135.B2
c 859	53.8	2.3	527	6	CA405139	CA405139	EL01N0529
860	53.8	2.3	593	4	BM143646	BM143646	saj47a09.
c 861	53.8	2.3	825	7	CO981254	CO981254	GM89010B2
c 862	53.6	2.3	446	2	AW113351	AW113351	MC798 mou
c 863	53.6	2.3	635	1	AU219747	AU219747	AU219747

c 864	53.6	2.3	816	7	CR530976	CR530976	CR530976
c 865	53.6	2.3	836	1	AI529553	AI529553	ui82a02.x
866	53.6	2.3	888	6	CA975538	CA975538	AGENCOURT
867	53.6	2.3	954	7	CO580598	CO580598	ILLUMIGEN
c 868	53.6	2.3	1014	9	CNS05PJQ	AL348047	Tetraodon
c 869	53.4	2.3	253	2	AW531318	AW531318	UI-R-C4-a
c 870	53.4	2.3	360	9	FR0015823	AL007029	F.rubripe
871	53.4	2.3	574	7	CN133765	CN133765	OX1_18_E0
872	53.4	2.3	629	6	CB927938	CB927938	ABAL_35_B
873	53.4	2.3	687	1	AU055875	AU055875	AU055875
874	53.4	2.3	733	9	CR501049	CR501049	Medicago
875	53.4	2.3	736	9	CR500903	CR500903	Medicago
c 876	53.4	2.3	784	7	CK265007	CK265007	EST711085
877	53.4	2.3	820	4	BG577461	BG577461	R77 MPIZ-
878	53.4	2.3	822	9	CR500725	CR500725	Medicago
c 879	53.4	2.3	875	9	CC692091	CC692091	OGLBU37TH
880	53.4	2.3	875	9	CC692097	CC692097	OGLBU37TV
881	53.4	2.3	945	4	BG167885	BG167885	602339857
c 882	53.2	2.3	552	2	AW351201	AW351201	GM210011A
c 883	53.2	2.3	552	6	CB399450	CB399450	OSTR221F2
c 884	53.2	2.3	552	6	CB399482	CB399482	OSTR221F2
c 885	53.2	2.3	700	2	BE190894	BE190894	sn80c04.y
c 886	53.2	2.3	738	4	BJ775701	BJ775701	BJ775701
887	53.2	2.3	743	2	BF236932	BF236932	602026557
c 888	53.2	2.3	769	4	BJ791007	BJ791007	BJ791007
889	53.2	2.3	873	7	CN167653	CN167653	AGENCOURT
890	53.2	2.3	914	7	CO645579	CO645579	ILLUMIGEN
c 891	53	2.3	467	1	AI665286	AI665286	605009C03
892	53	2.3	602	6	CA248078	CA248078	SCCCAM109
893	53	2.3	603	9	FR0007962	Z91772	F.rubripes
894	53	2.3	614	6	CA242675	CA242675	SCSFLL309
c 895	53	2.3	925	7	CN761277	CN761277	ID0AAA2DE
896	52.8	2.3	447	5	BU039808	BU039808	PP_LEa000
897	52.8	2.3	499	4	BI610180	BI610180	RH15147.5
898	52.8	2.3	514	5	BM952830	BM952830	952059E04
899	52.8	2.3	652	8	AZ945505	AZ945505	2M0206H23
c 900	52.8	2.3	672	4	BJ135701	BJ135701	BJ135701
c 901	52.8	2.3	755	4	BJ809035	BJ809035	BJ809035
c 902	52.6	2.3	573	8	AZ831866	AZ831866	2M0111C19
903	52.6	2.3	619	9	FR0007177	Z90987	F.rubripes
904	52.6	2.3	992	9	CNS038FN	AL232556	Tetraodon
c 905	52.4	2.3	464	9	CC693642	CC693642	OGUGK52TH
906	52.4	2.3	504	6	CA700350	CA700350	wkmlc.pk0
907	52.4	2.3	519	6	CA627167	CA627167	wlln.pk15
c 908	52.4	2.3	528	7	CV051393	CV051393	EST 10848
909	52.4	2.3	544	6	CA621946	CA621946	wlln.pk00
910	52.4	2.3	545	5	BQ483975	BQ483975	WHE3515_A
c 911	52.4	2.3	551	9	CG233803	CG233803	OGVCV89TH
912	52.4	2.3	573	7	CV053322	CV053322	EST 12770
913	52.4	2.3	593	7	CV053078	CV053078	EST 12526
914	52.4	2.3	619	9	FR0007182	Z90992	F.rubripes
c 915	52.4	2.3	623	9	CNS03MFA	AL250687	Tetraodon
c 916	52.4	2.3	638	7	CV051636	CV051636	EST 11091
c 917	52.4	2.3	666	1	AI158921	AI158921	uf05c02.x
c 918	52.2	2.3	443	8	CC029515	CC029515	3591_1_11
c 919	52.2	2.3	658	7	CO210550	CO210550	WS00918.B
920	52	2.2	272	9	CL175246	CL175246	104_380_1

921	52	2.2	343	4	BG182337	BG182337	RST1203	A
922	52	2.2	536	7	CF349411	CF349411	fc2486	e
923	52	2.2	582	5	BP217111	BP217111	BP217111	
924	52	2.2	631	6	CA111498	CA111498	SCAGLB107	
c 925	52	2.2	703	5	BQ475642	BQ475642	cicindela	
c 926	52	2.2	721	5	BQ262583	BQ262583	fz84dl2	x
927	52	2.2	803	1	AJ006537	AJ006537	AJ006537	
c 928	51.8	2.2	496	1	AI855338	AI855338	603014F06	
929	51.8	2.2	508	1	AI614365	AI614365	vi71h01	y
c 930	51.8	2.2	511	7	CO528524	CO528524	3530_1_18	
931	51.8	2.2	543	6	CB339758	CB339758	CA23EI03I	
c 932	51.8	2.2	574	6	CB339351	CB339351	CA23EI03I	
c 933	51.8	2.2	610	4	BI542629	BI542629	949020C07	
c 934	51.8	2.2	616	7	CO517693	CO517693	3530_1_11	
c 935	51.8	2.2	659	7	CF630818	CF630818	zmrws48	0
936	51.8	2.2	687	6	CB250778	CB250778	75 Aedes	
c 937	51.8	2.2	690	7	CF243936	CF243936	3530_1_25	
938	51.8	2.2	695	7	CK962027	CK962027	4076363	B
939	51.8	2.2	724	9	CL154714	CL154714	104_340_1	
940	51.8	2.2	748	6	CB954704	CB954704	AGENCOURT	
c 941	51.8	2.2	768	6	CB631476	CB631476	OSIIEb09A	
942	51.8	2.2	798	5	BM948419	BM948419	UI-M-EG0p	
c 943	51.8	2.2	822	7	CF633893	CF633893	zmrww00	0
944	51.8	2.2	827	7	CK370475	CK370475	zmrww005	
945	51.8	2.2	840	6	CB631477	CB631477	OSIIEb09A	
c 946	51.8	2.2	892	4	BG208263	BG208263	RST27755	
947	51.8	2.2	893	6	CA076965	CA076965	SCQGAM104	
948	51.8	2.2	949	3	AY105440	AY105440	Zea mays	
c 949	51.8	2.2	1049	2	BE573200	BE573200	601332887	
950	51.8	2.2	1419	9	CL965868	CL965868	OsIFCC012	
c 951	51.6	2.2	335	8	CC040482	CC040482	3591_1_13	
c 952	51.6	2.2	440	8	CC040369	CC040369	3591_1_13	
953	51.6	2.2	442	7	CN956527	CN956527	4027_5001	
c 954	51.6	2.2	454	8	CC040451	CC040451	3591_1_13	
c 955	51.6	2.2	461	8	CC042725	CC042725	3591_1_15	
c 956	51.6	2.2	545	6	CB505278	CB505278	ssalmgd50	
c 957	51.6	2.2	572	2	AW471171	AW471171	xu08h02	x
958	51.6	2.2	633	2	BF028687	BF028687	601763929	
c 959	51.6	2.2	667	7	CO519314	CO519314	3530_1_12	
c 960	51.6	2.2	671	4	BJ146707	BJ146707	BJ146707	
961	51.6	2.2	728	4	BI102440	BI102440	602889631	
c 962	51.6	2.2	729	9	CG436794	CG436794	OGVGU72TH	
c 963	51.6	2.2	777	9	CG267261	CG267261	OGWHF51TH	
964	51.6	2.2	781	6	CB683695	CB683695	OSJNEf12G	
c 965	51.6	2.2	834	7	CF634127	CF634127	zmrww00	0
966	51.6	2.2	854	1	AL931420	AL931420	AL931420	
c 967	51.6	2.2	899	9	CC618081	CC618081	OGLAX62TH	
968	51.6	2.2	1031	6	CA139432	CA139432	SCEQRT209	
969	51.4	2.2	494	9	CL572955	CL572955	OB_Ba001	
970	51.4	2.2	568	6	CD433794	CD433794	EL01N0315	
c 971	51.4	2.2	649	8	BZ726909	BZ726909	OGECF17TC	
972	51.4	2.2	654	7	CN150564	CN150564	WOUND1_70	
973	51.4	2.2	666	5	BQ753201	BQ753201	WHE4124	C
c 974	51.4	2.2	673	4	BJ783526	BJ783526	BJ783526	
975	51.4	2.2	673	9	CL537275	CL537275	OB_Ba004	
976	51.4	2.2	679	6	CA073196	CA073196	SCEPAM105	
c 977	51.4	2.2	690	1	AU216711	AU216711	AU216711	

c 978	51.4	2.2	702	4	BJ788990	BJ788990	BJ788990
979	51.4	2.2	707	8	BZ726916	BZ726916	OGECF17TM
c 980	51.4	2.2	708	4	BJ133121	BJ133121	BJ133121
c 981	51.4	2.2	709	4	BJ818107	BJ818107	BJ818107
c 982	51.4	2.2	763	6	CA135704	CA135704	SCJLRT102
c 983	51.4	2.2	799	6	CD871509	CD871509	AZO2.118G
984	51.4	2.2	919	9	CG445266	CG445266	OGTBF39TV
985	51.4	2.2	1127	7	CK028276	CK028276	AGENCOURT
986	51.2	2.2	532	9	CC733695	CC733695	OGUCO18TH
987	51.2	2.2	539	6	CD750145	CD750145	rv07c03.y
c 988	51.2	2.2	562	9	CC733706	CC733706	OGUCO18TV
989	51.2	2.2	565	5	BX676981	BX676981	BX676981
990	51.2	2.2	582	7	CO997967	CO997967	pam01-15m
991	51.2	2.2	707	7	CO070063	CO070063	GR_Ea260
c 992	51.2	2.2	784	7	CO070062	CO070062	GR_Ea260
c 993	51.2	2.2	790	7	CO084607	CO084607	GR_Ea01F
994	51.2	2.2	793	9	CG205456	CG205456	PUIAU44TD
c 995	51.2	2.2	1031	9	CC730025	CC730025	OGUDN62TV
996	51.2	2.2	1458	9	CL982528	CL982528	OsIFSC048
997	51	2.2	430	5	BP940165	BP940165	BP940165
998	51	2.2	586	9	FR0007952	Z91762	F.rubripes
c 999	51	2.2	596	5	BP036706	BP036706	BP036706
c1000	51	2.2	608	6	CB637106	CB637106	OSJNEa03E
1001	51	2.2	717	1	AF527714	AF527714	AF527714
c1002	51	2.2	750	6	CB646078	CB646078	OSJNEb08E
c1003	51	2.2	768	6	CB655823	CB655823	OSJNEc09J
c1004	51	2.2	769	6	CB680689	CB680689	OSJNEf05N
c1005	51	2.2	807	6	CB679495	CB679495	OSJNEf03B
c1006	51	2.2	809	6	CB679818	CB679818	OSJNEf03M
1007	51	2.2	810	6	CB680688	CB680688	OSJNEf05N
c1008	51	2.2	812	6	CB671618	CB671618	OSJNEe05E
1009	51	2.2	821	6	CB655822	CB655822	OSJNEc09J
c1010	51	2.2	829	6	CB666716	CB666716	OSJNEd13L
1011	50.8	2.2	265	7	CV052826	CV052826	EST 12274
c1012	50.8	2.2	494	7	CV047765	CV047765	EST 13082
1013	50.8	2.2	551	6	CA041628	CA041628	ssalplnb5
c1014	50.8	2.2	578	7	CO698343	CO698343	DG32-134j
1015	50.8	2.2	580	5	BP276996	BP276996	BP276996
1016	50.8	2.2	582	5	BP270998	BP270998	BP270998
1017	50.8	2.2	609	6	CD224613	CD224613	CCC1_35_F
c1018	50.8	2.2	647	4	BM269408	BM269408	MEST409-F
c1019	50.8	2.2	750	6	CB823924	CB823924	EST 5148
c1020	50.8	2.2	790	6	CB822697	CB822697	EST 3921
c1021	50.8	2.2	806	6	CB822464	CB822464	EST 3315
c1022	50.8	2.2	896	8	BZ652248	BZ652248	OGCBT21TM
c1023	50.8	2.2	932	7	CV245243	CV245243	WS0256.B2
1024	50.8	2.2	971	9	CG030644	CG030644	PUIEZ35TD
c1025	50.6	2.2	516	6	CA721277	CA721277	wdk9n.pk0
c1026	50.6	2.2	537	6	CD453688	CD453688	WHE0840_E
1027	50.6	2.2	539	7	CK893654	CK893654	SGP153746
c1028	50.6	2.2	564	4	BJ595115	BJ595115	BJ595115
1029	50.6	2.2	754	5	BQ752889	BQ752889	WHE4120_D
1030	50.6	2.2	769	9	CE543749	CE543749	tigr-gss-
1031	50.6	2.2	784	9	CG103720	CG103720	PUFQS48TD
c1032	50.6	2.2	828	6	CB621476	CB621476	OSIIEa07G
c1033	50.6	2.2	909	7	CO235179	CO235179	WS0263.B2
1034	50.6	2.2	1758	9	CL977417	CL977417	OsIFCC030

1035	50.4	2.2	404	4	BG730140	BG730140	de10c06.y
c1036	50.4	2.2	461	1	AI527401	AI527401	uj46c05.x
1037	50.4	2.2	463	5	BU046782	BU046782	PP_LEa002
1038	50.4	2.2	493	2	BE363468	BE363468	WS1_63_B0
c1039	50.4	2.2	494	6	CA403476	CA403476	EL01N0502
c1040	50.4	2.2	576	7	CF472330	CF472330	RTDS1_9_E
c1041	50.4	2.2	590	9	CL190425	CL190425	104_408_1
1042	50.4	2.2	591	6	CB927803	CB927803	ABA1_34_B
1043	50.4	2.2	628	2	BE356265	BE356265	DG1_123_A
1044	50.4	2.2	629	7	CV095362	CV095362	FAMU_USDA
1045	50.4	2.2	641	6	CB925748	CB925748	ABA1_23_C
1046	50.4	2.2	677	4	BM645987	BM645987	170006873
1047	50.4	2.2	680	2	BE126076	BE126076	DG1_65_E0
1048	50.4	2.2	681	4	BM300075	BM300075	MCR054H06
1049	50.4	2.2	682	2	BE362888	BE362888	DG1_90_B1
c1050	50.4	2.2	692	9	CL193419	CL193419	104_417_1
c1051	50.4	2.2	700	9	CL185025	CL185025	104_398_1
1052	50.4	2.2	766	7	CN139110	CN139110	OX1_16_B1
c1053	50.4	2.2	819	7	CF472392	CF472392	RTDS1_9_E
1054	50.4	2.2	858	7	CO162822	CO162822	FLD1_37_F
1055	50.4	2.2	1479	9	CL966467	CL966467	OsIFCC039
1056	50.4	2.2	1482	9	CL966466	CL966466	OsIFCC039
1057	50.4	2.2	1536	9	CL949054	CL949054	OsIFSB003
1058	50.2	2.2	476	6	CA117818	CA117818	SCBGLR104
c1059	50.2	2.2	505	9	CG782598	CG782598	1123051B1
c1060	50.2	2.2	523	7	CO110296	CO110296	GR_Eb004
c1061	50.2	2.2	523	7	CO131794	CO131794	GR_Eb44E
1062	50.2	2.2	530	2	AW677595	AW677595	DG1_8_E07
1063	50.2	2.2	583	7	CR529808	CR529808	CR529808
1064	50.2	2.2	614	2	BF144793	BF144793	601791473
c1065	50.2	2.2	665	4	BJ275225	BJ275225	BJ275225
1066	50.2	2.2	673	4	BM639164	BM639164	170006875
c1067	50.2	2.2	680	6	CB680895	CB680895	OSJNEf06G
1068	50.2	2.2	688	2	BE403580	BE403580	WHE0434_C
c1069	50.2	2.2	696	7	CR529807	CR529807	CR529807
c1070	50.2	2.2	736	6	CB650859	CB650859	OSJNEb15I
c1071	50.2	2.2	736	9	CW516566	CW516566	OP_Ba004
c1072	50.2	2.2	745	6	CB677705	CB677705	OSJNEe14P
1073	50.2	2.2	754	5	BX617512	BX617512	BX617512
c1074	50.2	2.2	755	6	CB643719	CB643719	OSJNEb04J
c1075	50.2	2.2	755	6	CB643721	CB643721	OSJNEb04J
c1076	50.2	2.2	765	6	CB651523	CB651523	OSJNEb16I
c1077	50.2	2.2	771	6	CB668190	CB668190	OSJNEd15O
c1078	50.2	2.2	778	6	CB643291	CB643291	OSJNEb03O
c1079	50.2	2.2	785	6	CB657829	CB657829	OSJNEc13H
c1080	50.2	2.2	800	6	CB643653	CB643653	OSJNEb04H
1081	50.2	2.2	811	6	CB657828	CB657828	OSJNEc13H
1082	50	2.2	488	5	BU047265	BU047265	PP_LEa002
c1083	50	2.2	543	7	CO120590	CO120590	GR_Eb024
c1084	50	2.2	675	8	BZ655726	BZ655726	OGCCX27TM
c1085	50	2.2	718	4	BJ295169	BJ295169	BJ295169
c1086	50	2.2	755	7	CO119232	CO119232	GR_Eb022
c1087	50	2.2	767	7	CO117573	CO117573	GR_Eb01H
c1088	50	2.2	819	9	CC609436	CC609436	OGWEC21TH
c1089	50	2.2	860	9	CG332048	CG332048	OG3CV53TH
c1090	50	2.2	862	9	CC660585	CC660585	OGUHJ18TH
1091	49.8	2.1	401	4	BI610047	BI610047	RH14915.5

1092	49.8	2.1	405	2	BB846514
1093	49.8	2.1	407	2	BB738955
c1094	49.8	2.1	509	6	CA400504
c1095	49.8	2.1	549	6	CA404237
1096	49.8	2.1	552	7	CF427347
c1097	49.8	2.1	567	6	CB397962
c1098	49.8	2.1	567	6	CB398012
c1099	49.8	2.1	604	9	CL159037
1100	49.8	2.1	617	8	BH801909
1101	49.8	2.1	641	6	CD233295
c1102	49.8	2.1	656	7	CO105005
1103	49.8	2.1	659	9	CL187944
1104	49.8	2.1	677	4	BI600040
1105	49.8	2.1	684	7	CN149641
1106	49.8	2.1	706	7	CN145147
c1107	49.8	2.1	721	9	CL187943
c1108	49.8	2.1	752	4	BJ783202
c1109	49.8	2.1	759	9	CG345428
1110	49.8	2.1	760	9	CG213435
c1111	49.8	2.1	833	7	CO078974
c1112	49.8	2.1	839	9	CG213425
1113	49.8	2.1	842	7	CO364746
1114	49.8	2.1	849	7	CO364666
1115	49.8	2.1	879	7	CO127109
1116	49.8	2.1	907	7	CO070408
c1117	49.8	2.1	938	7	CV236386
1118	49.6	2.1	314	6	CA695039
1119	49.6	2.1	418	5	BQ768447
1120	49.6	2.1	503	6	CA625114
1121	49.6	2.1	509	2	BF786568
c1122	49.6	2.1	559	6	CB398029
c1123	49.6	2.1	559	6	CB398045
c1124	49.6	2.1	633	4	BJ147155
1125	49.6	2.1	642	9	CL952976
1126	49.6	2.1	682	7	CV091309
c1127	49.6	2.1	685	4	BJ781077
1128	49.6	2.1	701	7	CR526982
1129	49.6	2.1	706	5	BX617038
c1130	49.6	2.1	714	7	CO119668
1131	49.6	2.1	715	4	BM575036
c1132	49.6	2.1	764	9	CG369437
1133	49.6	2.1	798	9	CG369451
1134	49.6	2.1	803	2	BF788917
1135	49.6	2.1	829	3	AY109290
1136	49.6	2.1	860	6	CA495127
c1137	49.6	2.1	904	9	CC703914
1138	49.4	2.1	551	4	BM419334
1139	49.4	2.1	622	6	CA265117
1140	49.4	2.1	626	6	CA273035
1141	49.4	2.1	650	7	CO816664
c1142	49.4	2.1	736	6	CB619162
c1143	49.4	2.1	754	6	CB619200
c1144	49.4	2.1	784	7	CO113301
c1145	49.4	2.1	791	7	CO118073
1146	49.4	2.1	793	7	CO112194
c1147	49.4	2.1	793	9	CG351341
1148	49.2	2.1	410	2	BB743553

BB846514	BB846514
BB738955	BB738955
CA400504	EL01N0405
CA404237	EL01N0514
CF427347	PH1_1_C12
CB397962	OSTR196G9
CB398012	OSTR196G9
CL159037	104_348_1
BH801909	1008122A0
CD233295	SS1_13_C0
CO105005	GR_Eb003
CL187944	104_404_1
BI600040	603251425
CN149641	WOUND1_64
CN145147	WOUND1_27
CL187943	104_404_1
BJ783202	BJ783202
CG345428	OGYBX66TH
CG213435	OGXCM76TV
CO078974	GR_Ea41I
CG213425	OGXCM76TH
CO364746	RTK1_21_C
CO364666	RTK1_21_C
CO127109	GR_Eb11I
CO070408	GR_Ea27G
CV236386	WS01223.B
CA695039	wlmk4.pk0
BQ768447	EBro08_SQ
CA625114	wlln.pk01
BF786568	602108517
CB398029	OSTR197A7
CB398045	OSTR197A7
BJ147155	BJ147155
CL952976	OsIRUA004
CV091309	NA1809_cD
BJ781077	BJ781077
CR526982	CR526982
BX617038	BX617038
CO119668	GR_Eb022
BM575036	170006589
CG369437	OGYAP21TH
CG369451	OGYAP21TV
BF788917	602104648
AY109290	Zea mays
CA495127	AGENCOURT
CC703914	OGUBW44TV
BM419334	R012D09_O
CA265117	SCRFR305
CA273035	SCEQRT3C0
CO816664	FA_SEa000
CB619162	OSIIEa03I
CB619200	OSIIEa03J
CO113301	GR_Eb013
CO118073	GR_Eb020
CO112194	GR_Eb004
CG351341	OGXAK06TH
BB743553	BB743553

1149	49.2	2.1	670	1	AJ774738	AJ774738	AJ774738
c1150	49.2	2.1	696	9	CC701513	CC701513	OGULT75TV
c1151	49.2	2.1	742	8	CC378191	CC378191	PUHSJ65TB
c1152	49.2	2.1	752	6	CB661740	CB661740	OSJNEd05A
1153	49.2	2.1	764	9	BX989346	BX989346	Reverse s
c1154	49.2	2.1	774	8	BZ727921	BZ727921	OGFCT54TM
c1155	49.2	2.1	799	8	CC339126	CC339126	OGOBC85TH
1156	49.2	2.1	826	9	CG318335	CG318335	OG0FG24TH
c1157	49.2	2.1	850	9	CG318346	CG318346	OG0FG24TV
c1158	49.2	2.1	858	7	CO518703	CO518703	3530_1_12
c1159	49.2	2.1	903	9	CG243251	CG243251	OGWBC25TH
c1160	49.2	2.1	916	9	CC658647	CC658647	OGTAL07TC
c1161	49.2	2.1	923	9	CC726252	CC726252	OGUGI94TV
1162	49.2	2.1	934	1	AI064363	AI064363	GH04745.5
c1163	49.2	2.1	981	2	AW940177	AW940177	GH04745.3
1164	49	2.1	372	2	BE425760	BE425760	WHE0316_C
1165	49	2.1	505	7	CO266931	CO266931	EK147954.
c1166	49	2.1	550	1	AU246308	AU246308	AU246308
1167	49	2.1	655	6	CB970156	CB970156	CAB10003_
1168	49	2.1	676	4	BJ071376	BJ071376	BJ071376
c1169	49	2.1	760	6	CB620857	CB620857	OSIIEa06F
c1170	49	2.1	768	6	CB970233	CB970233	CAB10003_
1171	49	2.1	866	6	CA481981	CA481981	AGENCOURT
1172	49	2.1	874	8	CC113815	CC113815	NDL.34M4.
c1173	48.8	2.1	413	7	CF649328	CF649328	3530_1_68
1174	48.8	2.1	456	8	BZ534563	BZ534563	OGALJ03TM
c1175	48.8	2.1	539	8	BZ534560	BZ534560	OGALJ03TC
1176	48.8	2.1	570	5	BP274123	BP274123	BP274123
1177	48.8	2.1	601	7	CV511561	CV511561	kc43h09.y
c1178	48.8	2.1	610	5	BX559661	BX559661	BX559661
c1179	48.8	2.1	645	9	CC608615	CC608615	OGUAR12TV
1180	48.8	2.1	723	7	CO363008	CO363008	RTK1_7_C0
1181	48.8	2.1	734	7	CV031446	CV031446	RTNACL1_1
1182	48.8	2.1	740	9	CC608604	CC608604	OGUAR12TH
c1183	48.8	2.1	788	9	CC647080	CC647080	OGNAF05TH
c1184	48.8	2.1	804	7	CO526636	CO526636	3530_1_17
c1185	48.8	2.1	805	8	BZ642226	BZ642226	OGAPA15TM
c1186	48.8	2.1	828	7	CO367803	CO367803	RTK1_36_E
c1187	48.8	2.1	862	9	CC660737	CC660737	OGLBT68TH
c1188	48.8	2.1	904	8	CC326984	CC326984	OGIAX93TV
1189	48.6	2.1	393	9	CL948532	CL948532	OsIFSB005
1190	48.6	2.1	527	4	BG052249	BG052249	RHIZ2_12_
c1191	48.6	2.1	532	5	BQ662175	BQ662175	HR01004u
1192	48.6	2.1	654	6	CA258723	CA258723	SCBGRT301
c1193	48.6	2.1	685	7	CF179609	CF179609	814592 MA
c1194	48.6	2.1	770	7	CR279298	CR279298	CR279298
1195	48.6	2.1	782	2	BF256192	BF256192	HVSMEf000
1196	48.6	2.1	883	7	CN019919	CN019919	AGENCOURT
1197	48.4	2.1	339	7	L33533	L33533	BNAESTF166
c1198	48.4	2.1	396	5	BQ540829	BQ540829	ps73a11.y
c1199	48.4	2.1	566	7	CF630060	CF630060	zmrws48_0
1200	48.4	2.1	579	9	CG118934	CG118934	PUIKV67TD
c1201	48.4	2.1	627	7	CO518792	CO518792	3530_1_12
c1202	48.4	2.1	631	1	AI711635	AI711635	605058E04
c1203	48.4	2.1	631	7	CO518008	CO518008	3530_1_11
c1204	48.4	2.1	638	6	CD721212	CD721212	VVB180H10
c1205	48.4	2.1	639	6	CD719709	CD719709	VVB164B11

c1206	48.4	2.1	644	6	CD719870	CD719870	VVB166A11
c1207	48.4	2.1	663	7	CF630588	CF630588	zmrws48_0
c1208	48.4	2.1	673	6	CD406404	CD406404	Gm_ck3123
c1209	48.4	2.1	675	7	CO521120	CO521120	3530_1_13
c1210	48.4	2.1	681	6	CD007604	CD007604	VVB073C12
c1211	48.4	2.1	681	6	CD713102	CD713102	VVB186C04
c1212	48.4	2.1	683	6	CD011026	CD011026	VVB118D02
c1213	48.4	2.1	687	6	CA202090	CA202090	SCSBFL104
c1214	48.4	2.1	715	4	BI967364	BI967364	GM830001B
c1215	48.4	2.1	720	8	BZ688359	BZ688359	OGDAD91TC
c1216	48.4	2.1	731	9	CC607404	CC607404	OGUFB75TH
1217	48.4	2.1	751	9	CG306324	CG306324	OG0GP22TH
c1218	48.4	2.1	753	8	BZ544993	BZ544993	OGAJC02TC
c1219	48.4	2.1	754	9	CC691465	CC691465	OGWDL65TH
c1220	48.4	2.1	809	9	CG298983	CG298983	OGYBC45TV
1221	48.4	2.1	836	9	CG211806	CG211806	OG0AC10TH
1222	48.4	2.1	844	2	BE055475	BE055475	GA_Ea003
c1223	48.4	2.1	861	7	CO238672	CO238672	WS00722.B
1224	48.4	2.1	876	7	CO070998	CO070998	GR_Ea28G
c1225	48.4	2.1	877	9	CG240612	CG240612	OGWAM46TV
c1226	48.4	2.1	896	9	CG211814	CG211814	OG0AC10TV
c1227	48.4	2.1	905	6	CD436944	CD436944	EL01N0365
1228	48.4	2.1	1027	9	CNS02KWD	AL202054	Tetraodon
1229	48.4	2.1	1101	9	CNS00BJK	AL057258	Drosophil
1230	48.4	2.1	1204	3	AY108318	AY108318	Zea mays
1231	48.2	2.1	344	9	CE594014	CE594014	tigr-gss-
c1232	48.2	2.1	459	7	CN072090	CN072090	1021025E0
1233	48.2	2.1	494	6	CA255455	CA255455	SCEPFL417
1234	48.2	2.1	623	5	BQ854360	BQ854360	QGB23A16.
c1235	48.2	2.1	640	5	BQ408246	BQ408246	GA_Ed000
1236	48.2	2.1	640	7	CF426997	CF426997	PH1_3_C05
1237	48.2	2.1	832	9	CG344045	CG344045	OGYAM82TV
1238	48.2	2.1	838	9	CG051217	CG051217	PUIAX51TD
c1239	48.2	2.1	844	9	CC619390	CC619390	OGUED54TV
1240	48.2	2.1	846	9	CC638581	CC638581	OGVBC68TH
c1241	48.2	2.1	940	9	CC638593	CC638593	OGVBC68TV
1242	48.2	2.1	1088	6	CA275165	CA275165	SCBFS103
1243	48	2.1	385	2	BE406114	BE406114	WHE0404_c
c1244	48	2.1	446	8	AZ047464	AZ047464	nbeb0094M
c1245	48	2.1	471	8	AQ866659	AQ866659	nbeb0028P
1246	48	2.1	492	2	BE357084	BE357084	DG1_146_G
c1247	48	2.1	601	7	CN444082	CN444082	Mdfw2001b
1248	48	2.1	609	9	CE605792	CE605792	tigr-gss-
1249	48	2.1	637	6	CD229006	CD229006	CCC1_11_D
1250	48	2.1	666	6	CD204458	CD204458	HS1_8_D09
c1251	48	2.1	672	9	CL389659	CL389659	RPCI44_28
c1252	48	2.1	677	8	AZ131490	AZ131490	OSJNBb011
1253	48	2.1	692	7	CF434115	CF434115	NIT1_32_A
c1254	48	2.1	728	7	CV234524	CV234524	WS01215.B
c1255	48	2.1	769	6	CD866162	CD866162	AZO2_102L
1256	48	2.1	1560	9	CL967117	CL967117	OsIFCC014
c1257	47.8	2.1	524	7	CO236941	CO236941	WS0071.B2
1258	47.8	2.1	534	8	BZ530624	BZ530624	OGALL21TC
c1259	47.8	2.1	575	4	BJ130201	BJ130201	BJ130201
c1260	47.8	2.1	586	1	AU217077	AU217077	AU217077
c1261	47.8	2.1	619	4	BJ140963	BJ140963	BJ140963
c1262	47.8	2.1	635	4	BJ136724	BJ136724	BJ136724

1263	47.8	2.1	679	7	CF387087	CF387087	RTDR1_10
1264	47.8	2.1	683	6	CA285250	CA285250	SCEQSD107
c1265	47.8	2.1	713	4	BJ132415	BJ132415	BJ132415
c1266	47.8	2.1	719	9	CC612397	CC612397	OGUCA43TV
1267	47.8	2.1	728	6	CA265146	CA265146	SCRFR305
c1268	47.8	2.1	729	6	CB619164	CB619164	OSIIEa03I
1269	47.8	2.1	732	7	CF385981	CF385981	RTDR1_7_E
1270	47.8	2.1	801	7	CF667004	CF667004	RTCNT1_27
1271	47.8	2.1	814	9	CG208272	CG208272	OGWGN76TH
1272	47.8	2.1	820	7	CO172600	CO172600	NDL1_30_E
c1273	47.8	2.1	826	8	BZ530629	BZ530629	OGALL21TM
c1274	47.8	2.1	833	8	BZ643693	BZ643693	OGCCE77TC
c1275	47.8	2.1	834	7	CV033205	CV033205	RTNACL1_3
1276	47.8	2.1	862	9	CG235352	CG235352	OGWIR47TV
1277	47.8	2.1	897	9	CG170061	CG170061	PUIGK25TB
c1278	47.8	2.1	912	9	CG208280	CG208280	OGWGN76TV
1279	47.8	2.1	939	9	CG308245	CG308245	OGVEF29TV
1280	47.8	2.1	972	9	CC630422	CC630422	OGLBS29TV
c1281	47.8	2.1	1101	9	CNS000D1	AL065414	Drosophil
1282	47.8	2.1	1458	9	CL973238	CL973238	OsIFCC042
1283	47.8	2.1	1476	9	CL959864	CL959864	OsIFCC036
c1284	47.6	2.1	574	7	CK095578	CK095578	UA14CPH12
c1285	47.6	2.1	615	6	CB872218	CB872218	HC07A12y
1286	47.6	2.1	644	6	CD235990	CD235990	SS1_25_B0
c1287	47.6	2.1	674	9	CL169524	CL169524	104_368_1
1288	47.6	2.1	674	9	CL192577	CL192577	104_415_1
1289	47.6	2.1	704	7	CF473082	CF473082	RTDS1_1_H
c1290	47.6	2.1	706	4	BI968444	BI968444	GM830005A
c1291	47.6	2.1	717	4	BJ284242	BJ284242	BJ284242
1292	47.6	2.1	870	9	CL977898	CL977898	OsIFCC044
c1293	47.6	2.1	910	7	CV243458	CV243458	WS02518.B
1294	47.4	2.0	367	1	AV693675	AV693675	AV693675
1295	47.4	2.0	367	1	AV694797	AV694797	AV694797
1296	47.4	2.0	367	1	AV696603	AV696603	AV696603
1297	47.4	2.0	367	1	AV696605	AV696605	AV696605
1298	47.4	2.0	367	1	AV697866	AV697866	AV697866
1299	47.4	2.0	367	1	AV698780	AV698780	AV698780
1300	47.4	2.0	367	1	AV698800	AV698800	AV698800
c1301	47.4	2.0	452	6	CB684060	CB684060	OSJNef13D
c1302	47.4	2.0	536	6	CB394655	CB394655	OSTR141F1
1303	47.4	2.0	556	2	BF080514	BF080514	231438_MA
c1304	47.4	2.0	592	6	CA134676	CA134676	SCJFRT106
c1305	47.4	2.0	694	6	CB664715	CB664715	OSJNEd10J
c1306	47.4	2.0	753	6	CB684061	CB684061	OSJNef13D
c1307	47.4	2.0	820	9	CC604209	CC604209	OGUEL94TH
c1308	47.4	2.0	905	9	CG308237	CG308237	OGVEF29TH
1309	47.4	2.0	1473	9	CL973231	CL973231	OsIFCC042
c1310	47.2	2.0	396	8	AQ843589	AQ843589	nbxb0024I
c1311	47.2	2.0	445	8	AQ868140	AQ868140	nbeb0021H
1312	47.2	2.0	585	5	BQ702373	BQ702373	NXSI_127
1313	47.2	2.0	634	7	CF471631	CF471631	RTDS1_4_B
1314	47.2	2.0	641	7	CF471539	CF471539	RTDS1_4_B
c1315	47.2	2.0	661	1	AI402259	AI402259	GH11333.3
1316	47.2	2.0	681	7	CN127822	CN127822	RHOH1_25
c1317	47.2	2.0	692	7	CF397219	CF397219	RTDS3_2_G
1318	47.2	2.0	723	7	CF478552	CF478552	RTWW3_20
1319	47.2	2.0	787	9	CG210062	CG210062	OGWGK05TH

c1320	47.2	2.0	800	6	CB971452
1321	47.2	2.0	801	7	CK130111
c1322	47.2	2.0	905	9	CG210073
1323	47.2	2.0	1092	9	CNS020K7
1324	47.2	2.0	1101	9	CNS0039G
c1325	47	2.0	216	6	CD944291
1326	47	2.0	216	6	CD946848
c1327	47	2.0	216	6	CD959938
1328	47	2.0	216	6	CF064465
1329	47	2.0	388	5	BX283268
1330	47	2.0	447	1	AA822117
1331	47	2.0	489	9	CL973113
1332	47	2.0	570	7	CO529692
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c1334	47	2.0	588	4	BI983739
c1335	47	2.0	598	1	AI964683
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1340	47	2.0	664	6	CA256133
1341	47	2.0	731	6	CA137836
c1342	47	2.0	776	9	CG949887
c1343	47	2.0	782	7	CK091254
1344	47	2.0	820	9	CG322167
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1355	46.8	2.0	556	7	CF393594
1356	46.8	2.0	569	7	CF429042
1357	46.8	2.0	575	5	BU100894
1358	46.8	2.0	578	4	BJ521530
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1360	46.8	2.0	597	2	BE593270
c1361	46.8	2.0	619	4	BJ239537
c1362	46.8	2.0	629	7	CO083786
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1367	46.8	2.0	758	7	CF666932
1368	46.8	2.0	778	7	CF393653
c1369	46.8	2.0	807	9	CG317189
c1370	46.8	2.0	865	9	CG350507
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CG949887	MBEGH16TF
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CG322158	OG3AP40TH
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CG317189	OGXDU28TH
CG350507	OG3AM53TV
CO645622	ILLUMIGEN
CN324479	AGENCOURT
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1379	46.6	2.0	627	5	BQ864555	BQ864555	QGC27A13.
1380	46.6	2.0	635	5	BU692265	BU692265	JM01037H1
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1382	46.6	2.0	672	7	CF403057	CF403057	RTWW1_24_
1383	46.6	2.0	680	7	CF402964	CF402964	RTWW1_24_
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c1385	46.6	2.0	700	6	CD876252	CD876252	AZO3.109B
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1399	46.4	2.0	542	4	BI801893	BI801893	H064C08 E
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1401	46.4	2.0	556	6	CB259745	CB259745	25-E9602-
c1402	46.4	2.0	564	7	CV233345	CV233345	WS01210.B
c1403	46.4	2.0	579	1	AV831789	AV831789	AV831789
1404	46.4	2.0	583	4	BG410775	BG410775	EM1_25_F0
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1410	46.4	2.0	662	5	BQ578302	BQ578302	WHE0301_D
c1411	46.4	2.0	680	6	CD373574	CD373574	WHE0425_A
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c1414	46.4	2.0	809	6	CB645026	CB645026	OSJNEB06H
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1416	46.4	2.0	817	7	CN520132	CN520132	GQ0106.B3
c1417	46.4	2.0	838	7	CV236341	CV236341	WS01223.B
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1420	46.4	2.0	1204	9	CNS016E2	AL106628	Drosophil
1421	46.4	2.0	1447	3	CNS0A460	BX826605	Arabidops
1422	46.4	2.0	1523	3	CNS0A40Y	BX827027	Arabidops
1423	46.2	2.0	164	7	T69701	T69701	yc44h12.r1
1424	46.2	2.0	286	8	BZ729579	BZ729579	OGEDD27TC
1425	46.2	2.0	330	2	BE187215	BE187215	NXNV_160_
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1427	46.2	2.0	514	5	BU990882	BU990882	HD05F08r
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1429	46.2	2.0	532	6	CB175070	CB175070	pk79e02.y
1430	46.2	2.0	532	8	BZ716462	BZ716462	OGEBF10TM
1431	46.2	2.0	533	2	BE187204	BE187204	NXNV_160_
1432	46.2	2.0	539	9	CC604739	CC604739	OGUJE18TV
c1433	46.2	2.0	568	8	AQ966294	AQ966294	LERIJ28TR

1434	46.2	2.0	587	8	BH383893	BH383893	AG-ND-180
c1435	46.2	2.0	598	9	CR501961	CR501961	Medicago
1436	46.2	2.0	611	8	AQ966292	AQ966292	LERIJ28TF
1437	46.2	2.0	634	6	CA013515	CA013515	HT08L06r
c1438	46.2	2.0	643	2	AW695243	AW695243	NF093A08S
c1439	46.2	2.0	651	1	AV927784	AV927784	AV927784
c1440	46.2	2.0	655	7	CO208672	CO208672	WS0097.B2
1441	46.2	2.0	658	5	BQ405465	BQ405465	GA_Ed008
c1442	46.2	2.0	666	7	CO252782	CO252782	WS00817.B
c1443	46.2	2.0	669	1	AV929760	AV929760	AV929760
c1444	46.2	2.0	678	9	CC604731	CC604731	OGUJE18TH
1445	46.2	2.0	687	5	BX255181	BX255181	BX255181
1446	46.2	2.0	697	8	BZ726996	BZ726996	OGEDC39TC
c1447	46.2	2.0	800	8	BZ714225	BZ714225	OGEBF10TC
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c1449	46.2	2.0	841	8	BZ727000	BZ727000	OGEDC39TM
1450	46.2	2.0	865	7	CR285323	CR285323	CR285323
c1451	46.2	2.0	870	2	BF275954	BF275954	GA_Eb002
c1452	46.2	2.0	950	9	CG921186	CG921186	MBELH04TF
1453	46.2	2.0	1548	9	CL963779	CL963779	OsIFCC038
c1454	46	2.0	428	6	CA930524	CA930524	MTU4CA.P2
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1464	46	2.0	1047	9	CNS0164P	AL106291	Drosophil
1465	46	2.0	1557	9	CL968520	CL968520	OsIFCC040
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1472	45.8	2.0	609	8	BH560246	BH560246	BOGUG40TF
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1476	45.8	2.0	771	9	CC604218	CC604218	OGUEL94TV
1477	45.8	2.0	797	2	BF621553	BF621553	HVSMEa001
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1480	45.8	2.0	1491	9	CL959867	CL959867	OsIFCC036
1481	45.6	2.0	514	4	BI748107	BI748107	ro65h11.y
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1497	45.6	2.0	817	7	CN763120	CN763120	ID0AAA6AF
c1498	45.6	2.0	827	8	BZ724654	BZ724654	OGFAB52TM
c1499	45.4	2.0	494	2	BE186818	BE186818	946012G11
c1500	45.4	2.0	499	9	CL593846	CL593846	OB_Ba005

ALIGNMENTS

RESULT 1

AY404343

LOCUS AY404343 1182 bp DNA linear GSS 12-DEC-2003

DEFINITION Homo sapiens HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY404343

VERSION AY404343.1 GI:39760320

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1182)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1182)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

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ORIGIN

Query Match 50.9%; Score 1180.4; DB 9; Length 1182;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 1181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2

AK050128

LOCUS AK050128 2197 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730018P11 product:hypothetical UDP-glucuronosyl and UDP-glucosyl transferase containing protein, full insert sequence.

ACCESSION AK050128

VERSION AK050128.1 GI:26340835

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,

Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2197)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully acknowledge. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .2197

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ORIGIN

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Matches 1201; Conservative 0; Mismatches 438; Indels 6; Gaps 2;

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Db      32 AGGGTCCCTTAGTGGGGCACAGCTCTTTAGGTGTGCAACCTGTGTGTCAGGGCTCCACATAT 91

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Qy     121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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AY404344

DEFINITION Pan troglodytes HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. -

VERSION AY404344.1 GI:39760321

SOURCE Pan troglodytes (chimpanzee).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302
 REFERENCE 2 (bases 1 to 1180)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
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RESULT 4

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DEFINITION  AGENCOURT_7594754 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6043558
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ACCESSION   BQ216829
VERSION     BQ216829.1  GI:20398229
KEYWORDS    EST.
SOURCE      Homo sapiens (human)

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ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 879)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13284 row: 1 column: 23
 High quality sequence start: 17
 High quality sequence stop: 671.

FEATURES Location/Qualifiers

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 Average insert size 2.5 kb. Library enriched for
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 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 36.8%; Score 853.2; DB 5; Length 879;
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Qy 780 CTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTA ACTCTGACTTTGCCTTTGATTTTG 839
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Db 1 CTCATCTTCTACTGAAAGCAGAGATGTGGTTCATTA ACTCTGACTTTGCCTTTGATTTTG 60

Qy 840 CTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAAC 899
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Db 61 CTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAAC 120

Qy 900 CAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTG 959
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Db 121 CAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTG 180

Qy 960 TGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACA 1019
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Db 181 TGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAATCTTCAAGGAGATGAACA 240

Qy 1020 ATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCA 1079
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Db 241 ATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTCTCATTGGCCCA 300
 Qy 1080 AAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCC 1139
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 Db 301 AAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCC 360
 Qy 1140 TGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGG 1199
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 Db 361 TGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGG 420
 Qy 1200 CCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACA 1259
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 Db 421 CCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACA 480
 Qy 1260 TGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAG 1319
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 Db 481 TGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTAGTTAAAGAAGCTCAAGGCAG 540
 Qy 1320 AGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAG 1379
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 Db 541 AGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAG 600
 Qy 1380 TGGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCT 1439
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 Db 601 TGGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCT 660
 Qy 1440 GGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGC 1499
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 Db 661 GGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGC 720
 Qy 1500 AGCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGG 1559
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 Db 721 AGCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGG 780
 Qy 1560 GGACTCTATGGCTTTGT-GGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCC 1618
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 Db 781 GGACTCTATGGCTTTGTGGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCTTGGGGCC 840
 Qy 1619 AGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTG 1656
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 Db 841 ACAAAGGGGAAGGAGACCTAAAGCCAGGTGCACCCTTG 878

RESULT 5

CN396938

LOCUS CN396938 759 bp mRNA linear.. EST 16-MAY-2004

DEFINITION 17000417785787 GRN_EB Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN396938

VERSION CN396938.1 GI:47384533

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 759)

AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,

Qy 421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA 480
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 Db 426 GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA 485
 Qy 481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
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 Db 486 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 545
 Qy 541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 600
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 Db 546 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC 605
 Qy 601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG 660
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 Db 606 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG 665
 Qy 661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
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 Db 666 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 725
 Qy 721 GTCTACATTTGACAACACCATCAAGGAACATTTTC 754
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 Db 726 GTCTACATTTGACAACACCATCAAGGAACATTTTC 759

RESULT 6
 CD050395

LOCUS CD050395 916 bp mRNA linear EST 09-MAY-2003
 DEFINITION AGENCOURT_13977999 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CD050395
 VERSION CD050395.1 GI:30487290
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 916)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jamie Thompson, University of WI
 cDNA Library Preparation: Gina Zastrow-Hayes
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDKM37 row: m column: 04
 High quality sequence start: 12
 High quality sequence stop: 721.
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 source 1. .916
 /organism="Homo sapiens"
 /mol_type="mRNA"

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/db_xref="taxon:9606"
/tissue_type="embryonic trophoblasts, made from WA01 stem
cells"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_173"
/note="Vector: pDONR201; Site_1: attP2; Site_2: attP1;
LIBR_PRIMING - oligo dT; METHOD - full-length enriched;
LIBR_PROVIDER - Bradfield"

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ORIGIN

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Query Match          31.8%; Score 738; DB 6; Length 916;
Best Local Similarity 95.0%; Pred. No. 7.2e-198;
Matches 795; Conservative 0; Mismatches 36; Indels 6; Gaps 3;

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Qy      1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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Db      54 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 113

Qy      61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCCT 120
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Db     114 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCCT 173

Qy     121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     174 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 233

Qy     181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
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Db     234 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 293

Qy     241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG 300
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Db     294 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG 353

Qy     301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     354 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGA 413

Qy     361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
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Db     414 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 473

Qy     421 GTTGCAGTGCAGTCATTTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA 480
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Db     474 GTTGCAGTGCAGTCATTTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA 533

Qy     481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
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Db     534 CTTGACAT-GTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 592

Qy     541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTGGGCTCTTTGGAATTTGGGCTACC 600
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Db     593 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTGGGCTCTTTGGAATTTGGGCTACC 652

Qy     601 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     653 AATCCCCTTGTCTTATGTTCCAGTATTCCGTTTCCTTGCTGACTGATCACATGGACTTCTG 712

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Qy      661 GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA 720
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Qy      721 GTCTACATTTGACAACACCATCAAGGAACA--TTTCACAGAAGGCTCTAGGCCAGTTTTG 778
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Db      773 GTCTACATTTGACAACACCATCCAAGGACATTTTTCACAGAGGGCTCTAGGGCCAGTTTT 832

Qy      779 TCTC---ATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTT 832
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RESULT 7

AY404345

LOCUS AY404345 1185 bp DNA linear GSS 12-DEC-2003

DEFINITION Mus musculus HCM1859 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY404345

VERSION AY404345.1 GI:39760322

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1185)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1185)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers
source 1. .1185
/organism="Mus musculus"
/mol_type="genomic DNA"
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gene <1. .>1185
/locus_tag="HCM1859"

ORIGIN

Query Match 31.6%; Score 733.8; DB 9; Length 1185;
Best Local Similarity 76.8%; Pred. No. 1.3e-196;
Matches 910; Conservative 0; Mismatches 272; Indels 3; Gaps 1;

Qy 458 ATGGATTCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAACTTTTGACTACTGT 517
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 Db 1 ATGGACTTCTTAAAAAATGAGAACTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGT 60

Qy 518 CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTTCACCTTCATTTC 577
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 Db 61 TCTTTGCTAATTGTTGAAAAGCTTGGGAACGATTTGTGTCCTTTCTCCCTTTCAATTT 120

Qy 578 GGCTCTTTGGAATTTGGGCTACCAA---TCCCCTTGTCTTATGTTCCAGTATTCGGTTCC 634
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 Db 121 AGCTATATGGACTTTGGGTTACCAAGCGCCCCCTTGTCTATGCTCCAGTGTATGGTTCT 180

Qy 635 TTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGT 694
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 Db 181 GGTCTAACTGACCAAATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTGAT 240

Qy 695 TTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTTC 754
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 Db 241 TTCTCCATGAAGCAAAGGGAAATCCTTTCTCAGTATGACAGCACTATCCAGGAGCATTTT 300

Qy 755 ACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATT 814
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 Db 301 GTGGAAGGCTCTCAGCCAGTGTTGTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTC 360

Qy 815 AACTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGA 874
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 Db 361 AACTCTGACTTTGCTTTGGATTTTGCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGA 420

Qy 875 GGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAATTCATTGCCAAG 934
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 Db 421 GGTTTACTGGACAAACCTGTTTCCAGCAATACCCCAAGACTTGGAGAATTTTATCTCTCAG 480

Qy 935 TTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAAT 994
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 Db 481 TTTGGAGACTCAGGTTTTGTCTTGTGGCCCTGGGCTCTATAGTGAGCATGATTCACTCC 540

Qy 995 CCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG 1054
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 Db 541 AAGGAAATTATTAAGGAGATGAACAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGG 600

Qy 1055 AAGTGTCACTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTG 1114
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Qy 1115 GACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCACCAC 1174
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 Db 661 GATTGGCTTCCACAGACTGACCTTCTAGCTCACCTAGCATTCTGTCTGTTTGTCACTCAT 720

Qy 1175 GGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCT 1234
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 Db 721 GGAGGGATGAACAGTGTGATGGAGGCTGTCCATCATGGAGTACCCATGGTGGGGATTCCA 780

Qy 1235 CTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCT 1294
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 Db 781 TTTTTTTTGGACCAACCTGAAAACATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTCT 840

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1353)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

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/strain="C57BL/6J"
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CDS

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FVSFLPFQFSYMDLGLPSAPLSYAPVYGSGLTDQMDFWGRVKNFLMFLDFSMKQREIL
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ORIGIN

Query Match 31.5%; Score 731.6; DB 3; Length 1353;
 Best Local Similarity 73.1%; Pred. No. 5.6e-196;
 Matches 981; Conservative 0; Mismatches 354; Indels 7; Gaps 3;

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Db      16 AGGGTCCCTTAGTGGGGCACAGCTCTTTAGGTGTGCAACCTGTGTGTCAGGGCTCCACATAT 75

Qy      61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTCT 120
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Db      76 TCTACAGATGGCAGCACATCGGCGTTGGCTTCTCATGAGCTTCCTTTTCTTGAGGTTAT 135

Qy      121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
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Qy      181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
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Qy      301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA 360
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Db      313 TTGGCGTCCACCTGAAGATCAGGAAAAGAAATTTGCTGATCTTAGGCATCGACTTACAGA 372

Qy      361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
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Qy      481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540

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Db 493 CTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGTTCTTTGCTAATTGTTGAAAAGCT 552
 Qy 541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACC 600
 Db 553 TGGGAAACGATTTGTGTCTTTCTTCCCTTTCAATTTAGCTATATGGACTTTGGGTTACC 612
 Qy 601 AA---TCCCCTTGTCTTATGTTCCAGTATTCCGTTCTTGCTGACTGATCACATGGACTT 657
 Db 613 AAGCGCCCCCTTGTCTATGCTCCAGTGTATGGTTCTGGTCTAACTGACCAAATGGACTT 672
 Qy 658 CTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACAT 717
 Db 673 CTGGGGCCGAGTGAAGAACTTTCTGATGTTCTTGATTTCTCCATGAAGCAAAGGGAAAT 732
 Qy 718 GCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTT 777
 Db 733 CCTTTCTCAGTATGACAGCACTATCCAGGAGCATTTTGTGGAAGGCTCTCAGCCAGTGTT 792
 Qy 778 GTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTT 837
 Db 793 GTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCAACTCTGACTTTGCTTTGGATTT 852
 Qy 838 TGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAA 897
 Db 853 TGCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGAGG-TTACTGGACAAACCTGTTCA 911
 Qy 898 ACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTCT 957
 Db 912 GCCAATACCCCAAGACTTGGAGAATTTTATCTCTCAGTTTGGGAGACTCAGGTTTTGTCTCT 971
 Qy 958 TGTGACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATCTTCAAGGAGATGAA 1017
 Db 972 TGTGGCCCTGGGCTCTATAGTGAGCATGATTGAGTCCAAGGAAATTATTAAGGAGATGAA 1031
 Qy 1018 CAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCC 1077
 Db 1032 CAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGGACATGTAAGACTTCTCATTGGCC 1091
 Qy 1078 CAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCT 1137
 Db 1092 CAAAGATGTGAGTTTGGCCCCAAATGTCAAATCATGGATTGGCTTCACAGACTGACCT 1151
 Qy 1138 CCTGGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGA 1197
 Db 1152 TCTAGCTCACCTAGCATTCTGTTTGTCACTCATGGAGGGATGAACAGTGTGATGGA 1211
 Qy 1198 GGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAA 1257
 Db 1212 GGCTGTCCATCATGGAGTACCCATGGTGGGGATTCCATTTTTTTTTTGACCAACCTGAAAA 1271
 Qy 1258 CATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTTAAAGAAGCTCAAGGC 1317
 Db 1272 CATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTATTAGCTACAGACGCTCAAGGC 1331
 Qy 1318 AGAGACATTGGCTCTTAAGATG 1339
 Db 1339

Qy 764 TCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAAGTCTGAC 823
 Db 121 TCTCAGCCAGTGTTGTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCAACTCTGAC 180

Qy 824 TTTGCCTTTGATTTTGTCTGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATG 883
 Db 181 TTTGCCTTGGATTTTGTCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGAGGTTTACTG 240

Qy 884 GAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAAGTTCATTGCCAAGTTTGGGGAC 943
 Db 241 GACAAACCTGTTTCAGCCAATACCCCAAGACTTGGAGGATTTTATCTCTCAGTTTGGAGAC 300

Qy 944 TCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGAGAATCCGGAAATC 1003
 Db 301 TCAGGTTTTGTCTTGTGGCCCTGGACTCTGTAGTGAGCATGATTCAGTCCAAGGAAATT 360

Qy 1004 TTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAC 1063
 Db 361 ATTAAGGAGATGAACAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGGACATGTAAG 420

Qy 1064 TGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTT 1123
 Db 421 AGTTCTCATTGGCCCAAAGATGTGAGTTTGGCCCAAATGTCAAATCATGGATTGGCTT 480

Qy 1124 CCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAG 1183
 Db 481 CCACAGATTGACCTTCTAGCTCACCTAGCATTCGTCTGTTTGTACCCATGGGGGGATG 540

Qy 1184 AATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGA 1243
 Db 541 AACAGTGTAATGGAGGCTGTCCATCATGGAGTACCAATGGTAGGGATTCCATTTTTTGA 600

Qy 1244 GACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAGTTTGGTGTCTTATTAGTTA 1303
 Db 601 GACCAACCTGAAAACATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTATTAGCTA 660

Qy 1304 AAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGA 1363
 Db 661 CAGACACTCAAGGCAGAGTCATTTTGGCTCACCATGAAAGAAGTCATAGAAGACCAGAGG 720

Qy 1364 TACAAGTCCGCGGCAGTGGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACA 1423
 Db 721 TACAAGACTGCAGCA-TGGCCTCCAAGTTATCAGGAAGTCCCACC--AATGACCCTGGC 777

Qy 1424 CAGCGGCTGGTGGGCTGGATTGACCACGTC-CTCCAGACAGGGGGCGCGACGCACCTCAA 1482
 Db 778 CAGAGGCTTGTGGGCTGGATTGATCACATCTTTGCAGACAGGGGGTGCAGCCCATCTCAA 837

Qy 1483 GCCCTATGTCTT-TCAGCAGCCCTGGCATGAGCAGTAC 1519
 Db 838 AGCATATGGCTTCCCAGCAGGCTTGGCATAACGAGTAC 875

RESULT 10

CN396939

LOCUS CN396939 510 bp mRNA linear EST 16-MAY-2004

DEFINITION 17000599940872 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN396939
 VERSION CN396939.1 GI:47384534
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 510)
 AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J and Stanton, L.W.
 TITLE Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 510 Std Error: 0.00.
 FEATURES Location/Qualifiers
 source 1. .510
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cell, retinoic acid and
 mitogen-treated hES cell line H7"
 /clone_lib="GRN_PRENEU"
 /note="oligo dT primed, full-length enriched cDNA library
 from hES cell line H7 (p29) maintained in feeder-free
 conditions. Embryoid bodies were generated in the presence
 of all-trans retinoic and mitogens."

ORIGIN

Query Match 21.8%; Score 506.4; DB 7; Length 510;
 Best Local Similarity 99.8%; Pred. No. 4.5e-132;
 Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1109 ATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTC 1168
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3 ATTGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTC 62
 Qy 1169 ACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGG 1228
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 63 ACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGG 122
 Qy 1229 ATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGT 1288
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 123 ATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGT 182
 Qy 1289 GTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATC 1348
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 183 GTTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATC 242
 Qy 1349 ATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCCAC 1408

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                |||
Db      243 ATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCCAC 302
Qy      1409 CCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGC 1468
                |||
Db      303 CCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGC 362
Qy      1469 GCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGAC 1528
                |||
Db      363 GCGACGCACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGCTCGAC 422
Qy      1529 GTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTG 1588
                |||
Db      423 GTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTG 482
Qy      1589 GGCATGGCTGTCTGGTGGCTGCGTGGGG 1616
                |||
Db      483 GGCATGGCTGTCTGGTGGCTGCGTGGGG 510

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RESULT 11

CR769328

LOCUS CR769328 717 bp mRNA linear EST 23-SEP-2004

DEFINITION DKFZp469O0528_r1 469 (synonym: pkidl) Pongo pygmaeus cDNA clone
DKFZp469O0528 5', mRNA sequence.

ACCESSION CR769328

VERSION CR769328.1 GI:52613343

KEYWORDS EST.

SOURCE Pongo pygmaeus (orangutan)

ORGANISM Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

REFERENCE 1 (bases 1 to 717)

AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.

TITLE Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,
Deutschenbaur,S., et al.)

JOURNAL Unpublished (2004)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
(Martinsried/Germany) within the cDNA-sequencing consortium of the
German Genome Project. This clone (DKFZp469O0528) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:

<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469O0528>

Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

source

Location/Qualifiers

1. .717

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="taxon:9600"

Db 664 GGAGCCCNATGGGGACATGCAGTCTACATTTGGACAACNCCNTCAAGGAGCATT 717

RESULT 12

BI559553

LOCUS BI559553 761 bp mRNA linear EST 05-SEP-2001

DEFINITION 603252894F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5295502 5', mRNA sequence.

ACCESSION BI559553

VERSION BI559553.1 GI:15446867

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 761)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL).

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11747 row: k column: 23

High quality sequence stop: 726.

FEATURES Location/Qualifiers

source

1. .761

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5295502"

/lab_host="DH10B"

/clone_lib="NIH_MGC_97"

/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 21.1%; Score 488.6; DB 4; Length 761;

Best Local Similarity 80.7%; Pred. No. 6.1e-127;

Matches 608; Conservative 0; Mismatches 139; Indels 6; Gaps 3;

Qy 8 CTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAGTGAGC 67

2-HYDROXYACYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR ;,
mRNA sequence.

ACCESSION AW173071

VERSION AW173071.1 GI:6439019

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 694)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 412.

FEATURES
source Location/Qualifiers
1. .694
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2663780"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 20.0%; Score 463.6; DB 2; Length 694;
Best Local Similarity 83.5%; Pred. No. 7.7e-120;
Matches 537; Conservative 0; Mismatches 105; Indels 1; Gaps 1;

Qy 268 TAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCACCTGAAGATCATCAAAG 327
|| |||| | ||| || || |||| | || | |||||

Db 643 TATAAAGAGAAGCAAAATTCATACAGGTATCCGGGTGGTTTTTCACCTAAGATCATCAAAA 584

Qy 328 AGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGGTGGCAGAGGAAAATT 387
|||| |||| ||| ||||| || | ||| | ||||| |||

Db 583 AGAA-TTAAGAAGCATTTTGATAGCTACATAGAAACAGCATTGGATGGCAGAAAAGAATC 525

Qy 388 TGAAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTCATTTTTTAAATAG 447
|||| | | || | | ||| |||| | ||||| ||| ||

Db 524 TGAAGCCCTTGTANAGCTAATGGAAATATTTGGGACTCAATGTAGTTATTTGCTAAGCAG 465

Db 178 ATCACCAAATTTGGAGACTCTGGTTTTGTCCTTGTAAAGCCTGGGGTCCATGGTGAGTTTC 119

Qy 986 TGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGG 1045
 || | | || | |||| ||||| ||||| || || |||||

Db 118 ATTCGGTCCCAGGAGTTCTCAAAGAGATGAATGCTGCCTTTGCTCATCTCCCTCAAGGG 59

Qy 1046 GTGATATGGAAGTGTCAGTGTTCTCATTGGCCCCAAAGATGTCCACCTGGCTGCAAA 1101
 ||||| ||||| | | ||||| ||||| || | ||| |||

Db 58 GTGATATGGAAGTATAATCCTTCTCATTGGCCCCAAAGACATCAAATTGGCCCCAAA 3

RESULT 15

AK052644

LOCUS AK052644 1723 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630011D02 product:hypothetical UDP-glucoronosyl and UDP-glucosyl transferase containing protein, full insert sequence.

ACCESSION AK052644

VERSION AK052644.1 GI:26095303

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE

4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE

5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1723)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .1723
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:D630011D02"
/db_xref="taxon:10090"
/clone="D630011D02"
/tissue_type="kidney"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"

misc_feature 1. .1723
/note="hypothetical UDP-glucoronosyl and UDP-glucosyl transferase containing protein (InterPro|IPR002213, evidence: InterPro)"

ORIGIN

Query Match 19.5%; Score 452.6; DB 3; Length 1723;
Best Local Similarity 69.1%; Pred. No. 1.5e-116;
Matches 649; Conservative 0; Mismatches 284; Indels 6; Gaps 2;

Qy 1 AGGGTCCCTTAGCCGGGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
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Db	41	AGGGTCCCTTAGTGGGGCACAGCTCTTTAGGTGTGCAACCTGTGTGTCAGGGCTCCACATAT	100
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	101	TCTACAGATGGCAGCACATCGGCGTTGGCTTCTCATGAGCTTCCTTTTCTTGAGGTTAT	160
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	161	TCTCTTGAGAGGCTGCAAAAATCCTGACTATATCTACACTGAGTGCAAGCCATTATATAGT	220
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	221	GATAAGCCGTGTGTCGCAAGTTCCTCATGAAGGTGGCCACAATGTGACCAAACCTCTTTA	280
Qy	241	CAAAAGAGGTCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Db	281	TGAAA---GTGCTAATATCCCAGATTTTAGAAAAGGAAAAACCATCATATCAAGTTATTAA	337
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTTCTTTCTGGA	360
Db	338	TTGGCGTCCACCTGAAGATCAGGAAAAGAAATTTGCTGATCTTAGGCATCGACTTACAGA	397
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
Db	398	AGAAATAACTTATGGCAGGTCCAAACATCACACCCTTCTAAAGATCCATCAATACTTTGG	457
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCTTTAAAGAATGAGAA	480
Db	458	GGACTTATGCAGTCAATTATTAAGCAGAAAGGACATCATGGACTTCTTAAAAAATGAGAA	517
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	518	CTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGTTCTTTGCTAATTGTTGAAAAGCT	577
Qy	541	TGGGAAGCCATTGTGCGCCATTCTTTCCTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	578	TGGGAAACGATTGTGTCTTTCTTCCCTTTCAATTTAGCTATATGGACTTTGGGTTACC	637
Qy	601	AA---TCCCCTTGCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTT	657
Db	638	AAGCGCCCCCTTGCTCTATGCTCCAGTGTATGGTTCTGGTCTAACTGACCAAATGGACTT	697
Qy	658	CTGGGGCCGAGTGAAGAAATTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACAT	717
Db	698	CTGGGGCCGAGTGAAGAACTTTCTGATGTTCTTGATTCTCCATGAAGCAAAGGGAAAT	757
Qy	718	GCAGTCTACATTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTT	777
Db	758	CCTTCTCAGTATGACAGCACTATCCAGGAGCATTTTGTGGAAGGCTCTCAGCCAGTGTT	817
Qy	778	GTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTT	837
Db	818	GTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCAACTCTGACTTTGCTTTGGATTT	877
Qy	838	TGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAA	897
Db	878	TGCTCGTCCCTGTTTCCCAACACAGTCTATGTGGGAGGTTTACTGGACAAACCTGTTCA	937

Qy 898 ACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTT 936
||| |||| |||| || || || | || ||
Db 938 GCCAATACCCCAAGTAAGTGACAAATTAGCTCTCACTTT 976

Search completed: February 15, 2005, 09:44:23
Job time : 6858 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 06:26:17 ; Search time 9715 Seconds
(without alignments)
11571.395 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 aggggtcccttagccgggcg.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
1	2320	100.0	2320	6	AX697213		AX697213 Sequence
2	2320	100.0	2320	9	AY358416		AY358416 Homo sapi
3	2310.2	99.6	2341	6	AX136141		AX136141 Sequence

	4	2310.2	99.6	2341	6	BD123523	BD123523	Secretary
	5	2310.2	99.6	2341	9	AK075383	AK075383	Homo sapi
	6	2102.8	90.6	2944	6	AX548037	AX548037	Sequence
	7	1578.8	68.1	2263	6	AX958403	AX958403	Sequence
	8	1281.6	55.2	2082	6	AX359921	AX359921	Sequence
	9	1281.6	55.2	2797	6	AX155211	AX155211	Sequence
	10	1281.6	55.2	2823	6	AX714604	AX714604	Sequence
	11	1281.6	55.2	2823	9	AK057066	AK057066	Homo sapi
	12	1280.6	55.2	2759	9	BC068446	BC068446	Homo sapi
	13	1280	55.2	2086	6	AX327327	AX327327	Sequence
	14	1212	52.2	1572	6	AX359923	AX359923	Sequence
	15	1147.8	49.5	2426	6	AR541778	AR541778	Sequence
c	16	957.6	41.3	88948	2	AC008947	AC008947	Homo sapi
	17	957.6	41.3	179513	9	AC016612	AC016612	Homo sapi
	18	944.8	40.7	1569	6	AX155213	AX155213	Sequence
	19	912.4	39.3	2210	10	AK128903	AK128903	Mus muscu
	20	912.2	39.3	2192	10	BC034837	BC034837	Mus muscu
	21	912.2	39.3	2196	10	BC022134	BC022134	Mus muscu
	22	910.8	39.3	2212	6	AX155214	AX155214	Sequence
	23	909.2	39.2	2228	10	BC025940	BC025940	Mus muscu
	24	905.8	39.0	1836	6	CQ726650	CQ726650	Sequence
	25	789	34.0	1569	6	AX155216	AX155216	Sequence
	26	595.4	25.7	148069	2	AC025476	AC025476	Homo sapi
	27	595.2	25.7	770	6	AX136483	AX136483	Sequence
	28	595.2	25.7	770	6	BD123723	BD123723	Secretary
	29	593.4	25.6	1842	6	AX747286	AX747286	Sequence
	30	593.4	25.6	1842	9	AK091977	AK091977	Homo sapi
	31	592.2	25.5	102255	2	AC026735	AC026735	Homo sapi
	32	575.4	24.8	5002	6	CQ842882	CQ842882	Sequence
	33	575.4	24.8	5002	9	AK125803	AK125803	Homo sapi
	34	573.6	24.7	125145	2	AC022136	AC022136	Homo sapi
	35	573.4	24.7	3108	9	BC035012	BC035012	Homo sapi
c	36	538.8	23.2	148069	2	AC025476	AC025476	Homo sapi
c	37	538.4	23.2	594	6	AX136632	AX136632	Sequence
c	38	538.4	23.2	594	6	BD123872	BD123872	Secretary
	39	471.2	20.3	1885	5	BC076709	BC076709	Xenopus t
	40	468.6	20.2	1835	5	CR760227	CR760227	Xenopus t
	41	444.8	19.2	88948	2	AC008947	AC008947	Homo sapi
	42	434.2	18.7	1839	5	BC082844	BC082844	Xenopus l
	43	433.6	18.7	105885	9	AC008860	AC008860	Homo sapi
c	44	320.6	13.8	156499	2	AC132893	AC132893	Mus muscu
	45	308.2	13.3	251769	2	AC117913	AC117913	Rattus no
	46	308	13.3	156499	2	AC132893	AC132893	Mus muscu
c	47	245.2	10.6	211178	10	AC139209	AC139209	Mus muscu
c	48	239.2	10.3	125145	2	AC022136	AC022136	Homo sapi
c	49	239.2	10.3	165304	9	AC112204	AC112204	Homo sapi
c	50	238.8	10.3	507	6	CQ337751	CQ337751	Sequence
c	51	220	9.5	277	6	CQ350335	CQ350335	Sequence
	52	174	7.5	1879	5	AF129809	AF129809	Gallus ga
	53	167.2	7.2	3598	10	AK128994	AK128994	Mus muscu
	54	167.2	7.2	4185	10	RNU07683	U07683	Rattus norv
	55	165.6	7.1	2633	10	RATCERUDPG	L21698	Rat ceramid
	56	164	7.1	2308	6	AX305987	AX305987	Sequence
	57	164	7.1	2308	10	MMGCGTEX	X92122	M.musculus
	58	164	7.1	3439	10	BC016885	BC016885	Mus muscu
	59	161.2	6.9	1593	4	AY135176	AY135176	Canis fam
	60	159.8	6.9	1609	4	AF129810	AF129810	Bos tauru

	61	158	6.8	291	6	CQ740738	CQ740738 Sequence
	62	156.8	6.8	464	11	G60984	G60984 SHGC-84035
c	63	156.8	6.8	69315	5	AL935277	AL935277 Zebrafish
	64	156.4	6.7	1671	4	RABUGT2BB	L01082 Oryctolagus
	65	156.2	6.7	239559	2	AC095531	AC095531 Rattus no
	66	152.6	6.6	1662	9	AF294902	AF294902 Macaca mu
	67	152.6	6.6	1753	9	AF016310	AF016310 Macaca fa
	68	152	6.6	1768	9	AF112113	AF112113 Macaca fa
	69	151.8	6.5	1832	4	RABUGT2BA	L01081 Oryctolagus
	70	151	6.5	2560	10	BC027200	BC027200 Mus muscu
	71	148.4	6.4	2897	4	RABUGT2BC	L01083 Oryctolagus
	72	148.2	6.4	2108	9	AF112112	AF112112 Macaca fa
	73	148	6.4	1716	10	RNUDPGT	Y00156 Rat mRNA fo
	74	148	6.4	1819	10	RATGRT	M31109 Rat UDP-glu
	75	148	6.4	2547	10	AF175221	AF175221 Cavia por
c	76	147.2	6.3	169025	2	CR545478	CR545478 Danio rer
c	77	147.2	6.3	179798	5	BX284110	BX284110 Zebrafish
	78	146.6	6.3	1825	10	AB034987	AB034987 Cavia por
	79	145.2	6.3	1961	6	AX401727	AX401727 Sequence
	80	145.2	6.3	1961	10	RATUDPGTP	M13506 Rat liver U
	81	144.8	6.2	2520	10	AB034988	AB034988 Cavia por
	82	144.6	6.2	1662	9	AF294901	AF294901 Macaca mu
	83	144.2	6.2	1584	6	AX497165	AX497165 Sequence
	84	144.2	6.2	2786	9	AK025587	AK025587 Homo sapi
	85	144.2	6.2	3006	6	AX497163	AX497163 Sequence
	86	143.2	6.2	1636	6	AX327326	AX327326 Sequence
	87	143.2	6.2	1647	9	AY542891	AY542891 Homo sapi
	88	143.2	6.2	2759	6	AX395164	AX395164 Sequence
	89	143.2	6.2	2966	6	AR447660	AR447660 Sequence
	90	143.2	6.2	2974	6	AX376454	AX376454 Sequence
	91	143.2	6.2	2974	9	AY358727	AY358727 Homo sapi
	92	143	6.2	2648	9	MFU91582	U91582 Macaca fasc
	93	142	6.1	1858	10	RATUDPA	M33746 Rat UDP glu
	94	141.8	6.1	336	6	AX307956	AX307956 Sequence
	95	141.8	6.1	1915	9	AF401657	AF401657 Macaca fa
	96	141.8	6.1	1947	10	RNU27518	U27518 Rattus norv
	97	141	6.1	1648	10	BC028262	BC028262 Mus muscu
	98	140.2	6.0	2595	10	BC058786	BC058786 Mus muscu
	99	140	6.0	2634	6	AX827435	AX827435 Sequence
	100	140	6.0	2634	10	RATUDPGTR	J02589 Rattus norv
	101	139.8	6.0	1584	10	AF184901	AF184901 Mus muscu
	102	139.8	6.0	1639	6	AX548042	AX548042 Sequence
	103	139.8	6.0	2585	10	BC048926	BC048926 Mus muscu
	104	139.8	6.0	125523	5	BX248385	BX248385 Zebrafish
	105	139.6	6.0	1896	10	BC078782	BC078782 Rattus no
	106	139.4	6.0	1858	10	MMUDPGT	X06358 Mouse mRNA
	107	139.4	6.0	1895	10	BC019487	BC019487 Mus muscu
	108	139.2	6.0	1855	6	CQ812293	CQ812293 Sequence
	109	139.2	6.0	1855	6	CQ870648	CQ870648 Sequence
	110	139.2	6.0	1855	6	AX336329	AX336329 Sequence
	111	139.2	6.0	1855	6	AX336696	AX336696 Sequence
	112	139.2	6.0	1855	6	AX409473	AX409473 Sequence
	113	139.2	6.0	1855	9	HUMUDPGTA	J05428 Human 3,4-c
	114	137.8	5.9	1831	10	RRUGTGENE	X57565 Rattus norv
	115	137.8	5.9	1891	10	BC057169	BC057169 Mus muscu
	116	137.8	5.9	1895	10	BC069923	BC069923 Mus muscu
	117	137.8	5.9	1903	10	BC015272	BC015272 Mus muscu

118	137	5.9	2125	5	BC078212	BC078212 Danio rer
119	136.8	5.9	1846	10	RNUDPGTR	X03478 Rat liver m
120	136.4	5.9	1692	9	BC075069	BC075069 Homo sapi
121	136.4	5.9	1844	10	RNU06273	U06273 Rattus norv
122	136.4	5.9	2107	6	AR168316	AR168316 Sequence
123	136.4	5.9	2107	9	HSU59209	U59209 Homo sapien
124	136.4	5.9	2172	6	CQ850790	CQ850790 Sequence
125	136.4	5.9	2172	9	AK127970	AK127970 Homo sapi
126	136.4	5.9	2448	6	AX335823	AX335823 Sequence
127	136.4	5.9	2448	6	AX770547	AX770547 Sequence
128	136.4	5.9	2448	9	HSU30930	U30930 Human UDP-G
129	136	5.9	1766	9	BC030974	BC030974 Homo sapi
130	136	5.9	1854	6	BD229166	BD229166 Genotype
131	136	5.9	1854	6	AR349418	AR349418 Sequence
132	133.8	5.8	1650	6	BD260955	BD260955 Carbohydr
133	133.8	5.8	1650	6	AX040087	AX040087 Sequence
134	133.8	5.8	1894	9	HSU62899	U62899 Human ceram
135	133.6	5.8	1976	5	BX936208	BX936208 Gallus ga
136	133.4	5.8	1760	6	CQ727328	CQ727328 Sequence
137	133.4	5.8	1766	9	HSA6054	AJ006054 Homo sapi
138	132	5.7	1614	6	AX958396	AX958396 Sequence
139	131.8	5.7	1851	9	AF177272	AF177272 Homo sapi
140	131.8	5.7	2093	5	BC076044	BC076044 Danio rer
141	131.6	5.7	1846	10	RNU06274	U06274 Rattus norv
142	131.6	5.7	2079	9	HSAJ5162	AJ005162 Homo sapi
143	131.6	5.7	2092	6	BD229135	BD229135 Genotype
144	131.6	5.7	2092	6	AR349387	AR349387 Sequence
145	131.6	5.7	2129	9	BC026264	BC026264 Homo sapi
146	130.6	5.6	1649	9	BC069441	BC069441 Homo sapi
147	130.6	5.6	2818	4	OCU72742	U72742 Oryctolagus
148	130	5.6	2097	9	AF064200	AF064200 Homo sapi
149	130	5.6	2123	6	AX410640	AX410640 Sequence
150	130	5.6	2123	9	HSU06641	U06641 Human UDP g
151	129	5.6	1722	9	AF016492	AF016492 Homo sapi
152	129	5.6	2799	6	AX411112	AX411112 Sequence
153	129	5.6	2799	9	HSUGT2BIO	X63359 H.sapiens U
154	128.6	5.5	1500	9	AF177274	AF177274 Homo sapi
155	128.4	5.5	1976	6	BD229238	BD229238 Genotype
156	128.4	5.5	1976	6	AR349490	AR349490 Sequence
157	128.4	5.5	2075	9	AF072223	AF072223 Macaca fa
158	128.4	5.5	2090	6	AX410646	AX410646 Sequence
159	128.4	5.5	2090	9	HSU08854	U08854 Human UDP g
160	128.4	5.5	2091	9	AF081793	AF081793 Homo sapi
161	128.4	5.5	2092	9	AF548389	AF548389 Homo sapi
162	128.4	5.5	2114	9	AF180322	AF180322 Homo sapi
163	128.2	5.5	1822	5	BC075289	BC075289 Xenopus t
164	128.2	5.5	3062	10	BC028826	BC028826 Mus muscu
165	127.6	5.5	1413	6	AR208679	AR208679 Sequence
166	127.6	5.5	1413	6	AR490895	AR490895 Sequence
167	125.2	5.4	2093	6	AX411198	AX411198 Sequence
168	125.2	5.4	2093	9	HSUDPGT	Y00317 Human mRNA
169	124.8	5.4	2816	4	AF039138	AF039138 Felis cat
170	124.8	5.4	2821	4	AF039137	AF039137 Felis cat
171	123.8	5.3	1895	5	BC075892	BC075892 Danio rer
172	122.4	5.3	2103	10	BC025795	BC025795 Mus muscu
173	121.6	5.2	1602	9	AF360121	AF360121 Macaca mu
174	121.6	5.2	2349	4	AB010872	AB010872 Felis cat

175	120.8	5.2	1590	4	AF011902	AF011902 Oryctolag
176	120.6	5.2	1224	6	AX958404	AX958404 Sequence
177	120	5.2	1647	9	AF104339	AF104339 Macaca fa
178	119.6	5.2	1587	4	CFA290948	AJ290948 Canis fam
179	119.6	5.2	2342	9	AY435136	AY435136 Homo sapi
180	119.6	5.2	2351	6	CQ720471	CQ720471 Sequence
181	119.6	5.2	2351	6	AX706961	AX706961 Sequence
182	119.6	5.2	2351	6	AX707891	AX707891 Sequence
183	119.6	5.2	2351	9	HUMHUGBR1	M57899 Human bilir
184	119.2	5.1	1621	9	AF104338	AF104338 Macaca fa
185	119	5.1	1961	5	BC055635	BC055635 Danio rer
186	118.8	5.1	2396	9	AF104336	AF104336 Macaca fa
187	117.6	5.1	2339	9	AY435141	AY435141 Homo sapi
188	117.6	5.1	2440	9	AF104337	AF104337 Macaca fa
189	116.8	5.0	1602	9	AY029169	AY029169 Macaca mu
190	116.2	5.0	2196	10	AY227201	AY227201 Mus muscu
191	116	5.0	2388	9	BC019861	BC019861 Homo sapi
192	115.8	5.0	2422	6	AX336711	AX336711 Sequence
193	115.8	5.0	2422	6	AX409459	AX409459 Sequence
194	115.8	5.0	2422	9	HUMUGT1FA	J04093 Homo sapien
195	114.6	4.9	2216	10	AY435129	AY435129 Rattus no
196	114.4	4.9	2345	9	AY435138	AY435138 Homo sapi
197	114.4	4.9	2345	9	AY435140	AY435140 Homo sapi
198	114.2	4.9	2333	9	AY435142	AY435142 Homo sapi
199	113.2	4.9	2392	9	S55985	S55985 Homo sapien
200	112.8	4.9	2345	9	AY435139	AY435139 Homo sapi
201	112.8	4.9	2368	9	HUMHUGBR2	M57951 Human bilir
202	112.6	4.9	1593	9	HSU89508	U89508 Human UDP-g
203	112.6	4.9	2003	9	AK025403	AK025403 Homo sapi
204	112.6	4.9	2333	9	AY435137	AY435137 Homo sapi
205	112.6	4.9	2390	9	BC069210	BC069210 Homo sapi
206	112.6	4.9	2423	9	BC020971	BC020971 Homo sapi
207	111.8	4.8	1590	4	AB008677	AB008677 Bos tauru
208	111.8	4.8	2219	10	AY435131	AY435131 Rattus no
209	111.4	4.8	2320	6	AX286762	AX286762 Sequence
210	111.4	4.8	2320	6	AX286764	AX286764 Sequence
211	111.4	4.8	2320	6	AX356964	AX356964 Sequence
212	111.4	4.8	2320	9	AF056188	AF056188 Homo sapi
213	111.4	4.8	2333	9	AY435144	AY435144 Homo sapi
214	111.4	4.8	2405	9	BC058844	BC058844 Homo sapi
215	111.4	4.8	2585	6	CQ796153	CQ796153 Sequence
216	111.4	4.8	2585	6	CQ796154	CQ796154 Sequence
217	111.4	4.8	2585	6	CQ796155	CQ796155 Sequence
218	111	4.8	1593	9	AF030310	AF030310 Homo sapi
219	111	4.8	1593	9	HSU89507	U89507 Human UDP-g
220	111	4.8	2333	9	AY435143	AY435143 Homo sapi
221	111	4.8	2363	9	AF462267	AF462267 Homo sapi
222	111	4.8	2394	9	AF462268	AF462268 Homo sapi
223	109.8	4.7	2216	10	AY435135	AY435135 Rattus no
224	109.8	4.7	2241	10	AF461735	AF461735 Rattus no
225	109.6	4.7	1655	5	PPL249081	AJ249081 Pleuronec
226	109.6	4.7	2287	4	AB018477	AB018477 Ovis arie
227	109.6	4.7	211178	10	AC139209	AC139209 Mus muscu
228	109.2	4.7	241472	5	BX005027	BX005027 Zebrafish
c 229	108.8	4.7	154733	2	AC127462	AC127462 Danio rer
c 230	108.8	4.7	247221	2	BX470211	BX470211 Danio rer
231	108.4	4.7	2284	10	AF461736	AF461736 Rattus no

232	108.2	4.7	2194	10	MUSUGTBR	L02333 Murine bili
233	108.2	4.7	2215	10	S64760	S64760 UGTBr1=UDP-
234	108.2	4.7	2224	10	AY227194	AY227194 Mus muscu
235	108	4.7	2190	10	AY227200	AY227200 Mus muscu
236	108	4.7	2203	10	BC019434	BC019434 Mus muscu
237	108	4.7	2215	10	AK128918	AK128918 Mus muscu
238	106.8	4.6	2231	10	AY435128	AY435128 Rattus no
239	106.8	4.6	2239	10	RNU20551	U20551 Rattus norv
240	106.6	4.6	2219	10	AY435134	AY435134 Rattus no
241	106.6	4.6	2225	10	AY435130	AY435130 Rattus no
242	106.6	4.6	2282	10	AF461738	AF461738 Rattus no
243	106.6	4.6	2285	10	BC078732	BC078732 Rattus no
244	105.4	4.5	2194	10	AB094481	AB094481 Mus muscu
245	105.4	4.5	2203	10	AY227196	AY227196 Mus muscu
246	105.2	4.5	1968	5	PPUGTMRN	X74116 P.platessa
247	105	4.5	1765	10	RATUDPGTA	M34007 Rat bilirub
248	104.8	4.5	2155	10	MUSUGTP	L27122 Mus musculu
249	104.8	4.5	2236	5	AB120133	AB120133 Pleuronec
250	104	4.5	151144	5	BX323575	BX323575 Zebrafish
251	103.8	4.5	2219	10	AY435132	AY435132 Rattus no
252	103.8	4.5	2297	10	AF461734	AF461734 Rattus no
253	103.4	4.5	2037	4	OCU09101	U09101 Oryctolagus
254	103.2	4.4	2193	10	AY227199	AY227199 Mus muscu
255	101.6	4.4	1584	6	CQ586740	CQ586740 Sequence
256	101.6	4.4	1602	10	D87866	D87866 Mus musculu
257	101.6	4.4	1619	3	AY070934	AY070934 Drosophil
258	101.6	4.4	2211	10	AY227195	AY227195 Mus muscu
c 259	101.6	4.4	3650	6	CQ586739	CQ586739 Sequence
c 260	101.6	4.4	164386	3	AC006491	AC006491 Drosophil
c 261	101.6	4.4	210298	3	AE003690	AE003690 Drosophil
262	100.8	4.3	2332	4	AB018478	AB018478 Ovis arie
263	100	4.3	1634	10	MMU09930	U09930 Mus musculu
c 264	100	4.3	24145	2	AC014455	AC014455 Drosophil
265	98.8	4.3	1212	6	CQ597654	CQ597654 Sequence
266	98.8	4.3	1704	6	CQ600372	CQ600372 Sequence
267	98.8	4.3	1980	3	BT006007	BT006007 Drosophil
268	98.8	4.3	1987	3	AY060891	AY060891 Drosophil
c 269	98.8	4.3	3212	6	CQ597653	CQ597653 Sequence
270	98.8	4.3	4357	6	CQ600371	CQ600371 Sequence
271	98.8	4.3	24145	2	AC014455	AC014455 Drosophil
272	98.8	4.3	164386	3	AC006491	AC006491 Drosophil
273	98.8	4.3	210298	3	AE003690	AE003690 Drosophil
274	98.4	4.2	2290	10	BC026561	BC026561 Mus muscu
275	98.4	4.2	2303	10	BC069940	BC069940 Mus muscu
276	97.6	4.2	1458	6	CQ590931	CQ590931 Sequence
277	97.6	4.2	3458	6	CQ590930	CQ590930 Sequence
278	97.6	4.2	37688	2	AL513222	AL513222 Drosophil
279	97.6	4.2	37688	3	DMCEG0003	AL031863 Drosophil
280	97.6	4.2	95850	2	AC020063	AC020063 Drosophil
281	97.6	4.2	154985	3	AC004641	AC004641 Drosophil
c 282	97.6	4.2	160338	3	AC099021	AC099021 Drosophil
c 283	97.6	4.2	272948	3	AE003805	AE003805 Drosophil
284	97	4.2	1593	10	D83796	D83796 Rat UGT1 mR
285	97	4.2	2216	10	AY435133	AY435133 Rattus no
286	97	4.2	2343	10	AF461737	AF461737 Rattus no
287	96.8	4.2	1596	10	D87867	D87867 Mus musculu
288	96.8	4.2	2265	10	AY227197	AY227197 Mus muscu

289	96.8	4.2	2300	10	MMU16818	U16818 Mus musculu
290	96.8	4.2	120848	2	AC007801	AC007801 Drosophil
291	95.6	4.1	735	6	AR252918	AR252918 Sequence
292	95.4	4.1	1927	10	RATUDPGT	J02612 Rat UDP-glu
293	95.2	4.1	2248	10	AY227198	AY227198 Mus muscu
c 294	94.6	4.1	168062	2	AC012857	AC012857 Drosophil
295	94.6	4.1	172479	3	AC006590	AC006590 Drosophil
296	94.6	4.1	260027	3	AE003659	AE003659 Drosophil
297	94	4.1	2055	4	OCU09030	U09030 Oryctolagus
298	93.4	4.0	1560	6	CQ586749	CQ586749 Sequence
c 299	93.4	4.0	3828	6	CQ586748	CQ586748 Sequence
300	93	4.0	1652	6	CQ580647	CQ580647 Sequence
301	93	4.0	1766	3	AY070917	AY070917 Drosophil
c 302	93	4.0	3991	6	CQ580646	CQ580646 Sequence
c 303	93	4.0	14112	6	CQ592361	CQ592361 Sequence
c 304	93	4.0	19914	2	AC018009	AC018009 Drosophil
305	93	4.0	177339	3	AC008231	AC008231 Drosophil
c 306	93	4.0	305150	3	AE003453	AE003453 Drosophil
307	92.8	4.0	662	6	AX525627	AX525627 Sequence
308	91.8	4.0	642	6	AX526169	AX526169 Sequence
309	91.6	3.9	662	6	AX525915	AX525915 Sequence
310	91.2	3.9	1662	9	BC053576	BC053576 Homo sapi
311	91	3.9	1648	6	CQ609717	CQ609717 Sequence
312	91	3.9	1692	3	AY118747	AY118747 Drosophil
313	88.8	3.8	1673	3	AY071256	AY071256 Drosophil
c 314	88.8	3.8	5278	6	CQ611354	CQ611354 Sequence
c 315	88.8	3.8	77707	2	AC014787	AC014787 Drosophil
c 316	88.8	3.8	177480	3	AC008287	AC008287 Drosophil
c 317	88.8	3.8	225974	3	AE003778	AE003778 Drosophil
318	88.2	3.8	2484	10	RATUGT	J05132 Rat 3-methy
319	87.4	3.8	1595	6	CQ586224	CQ586224 Sequence
320	86.2	3.7	874	6	AX421573	AX421573 Sequence
321	85.2	3.7	3716	6	CQ614606	CQ614606 Sequence
322	82.6	3.6	1572	6	CQ612552	CQ612552 Sequence
323	82.6	3.6	3572	6	CQ612551	CQ612551 Sequence
324	82.6	3.6	60144	2	AC019798	AC019798 Drosophil
c 325	82.6	3.6	91685	2	AC005121	AC005121 Drosophil
326	82.6	3.6	175413	3	AC093097	AC093097 Drosophil
327	82.6	3.6	262525	3	AE003652	AE003652 Drosophil
c 328	80.8	3.5	4016	6	CQ586223	CQ586223 Sequence
c 329	80.8	3.5	163325	3	AC008309	AC008309 Drosophil
c 330	80.8	3.5	167475	3	AC016132	AC016132 Drosophil
331	80.8	3.5	220936	2	AC020256	AC020256 Drosophil
c 332	80.8	3.5	241480	3	AE003734	AE003734 Drosophil
333	80.6	3.5	1593	6	CQ613314	CQ613314 Sequence
334	80.6	3.5	3659	6	CQ613313	CQ613313 Sequence
335	80.6	3.5	174677	3	AC018479	AC018479 Drosophil
336	80.6	3.5	193248	3	AC007752	AC007752 Drosophil
337	80.6	3.5	221239	3	AE003697	AE003697 Drosophil
c 338	80.6	3.5	324288	2	AC017336	AC017336 Drosophil
339	80	3.4	170142	9	AP002383	AP002383 Homo sapi
340	80	3.4	174742	2	AC016896	AC016896 Homo sapi
341	80	3.4	195466	2	AC032024	AC032024 Homo sapi
342	79.4	3.4	1413	6	CQ611790	CQ611790 Sequence
343	79.4	3.4	2820	6	CQ611355	CQ611355 Sequence
344	79.2	3.4	7218	6	I66494	I66494 Sequence 14
345	78.8	3.4	804	6	CQ727942	CQ727942 Sequence

346	78.8	3.4	1988	3	AY069392	AY069392 Drosophil
347	78.8	3.4	2437	3	AY071467	AY071467 Drosophil
348	78.6	3.4	678	6	AX526170	AX526170 Sequence
c 349	78.6	3.4	235952	2	AC110101	AC110101 Rattus no
c 350	78.6	3.4	256974	2	AC095475	AC095475 Rattus no
c 351	78	3.4	195466	2	AC032024	AC032024 Homo sapi
352	77.8	3.4	5205	6	CQ609716	CQ609716 Sequence
c 353	77.8	3.4	128469	2	AC020029	AC020029 Drosophil
354	77.8	3.4	172061	3	AC009203	AC009203 Drosophil
355	77.8	3.4	232737	3	AE003660	AE003660 Drosophil
356	77.2	3.3	189	6	CQ740741	CQ740741 Sequence
357	77	3.3	1352	10	MMGCGTEX1	X92123 M.musculus
358	77	3.3	2023	10	MMCGT2	U48892 Mus musculu
359	77	3.3	202752	2	AC111106	AC111106 Mus muscu
360	76.6	3.3	696	6	CQ734321	CQ734321 Sequence
361	76.4	3.3	169056	2	CR381587	CR381587 Danio rer
362	74.6	3.2	603	6	AX401758	AX401758 Sequence
363	74.6	3.2	603	10	S56937	S56937 3-methylcho
364	74	3.2	582	6	CQ458675	CQ458675 Sequence
365	73.8	3.2	4389	2	AC014898	AC014898 Drosophil
c 366	73.8	3.2	171334	3	AC007477	AC007477 Drosophil
c 367	73.8	3.2	196516	3	AC013450	AC013450 Drosophil
368	73.8	3.2	280240	3	AE003786	AE003786 Drosophil
c 369	73.2	3.2	237028	2	BX000470	BX000470 Danio rer
370	72.2	3.1	1443	9	HSCGT01	U31353 Human UDP-G
371	72.2	3.1	149028	9	AC122938	AC122938 Homo sapi
372	72	3.1	293	6	CQ427045	CQ427045 Sequence
373	72	3.1	439	6	CQ417459	CQ417459 Sequence
374	71.2	3.1	1681	3	AF324465	AF324465 Bombyx mo
375	70.8	3.1	601	6	AX401757	AX401757 Sequence
376	70.8	3.1	601	10	S56936	S56936 bilirubin-s
377	70.2	3.0	246176	2	AC114845	AC114845 Rattus no
378	69.4	3.0	1680	6	CQ586665	CQ586665 Sequence
379	69.4	3.0	1781	3	AY051661	AY051661 Drosophil
380	69.4	3.0	1782	6	CQ586689	CQ586689 Sequence
c 381	69.4	3.0	3741	6	CQ586664	CQ586664 Sequence
c 382	69.4	3.0	3849	6	CQ586688	CQ586688 Sequence
c 383	69.4	3.0	30221	2	AC014454	AC014454 Drosophil
c 384	69.4	3.0	165136	3	AC007645	AC007645 Drosophil
385	69.2	3.0	1491	6	CQ581757	CQ581757 Sequence
386	69.2	3.0	3784	6	CQ581756	CQ581756 Sequence
c 387	68.6	3.0	3595	6	CQ613379	CQ613379 Sequence
c 388	68.6	3.0	174677	3	AC018479	AC018479 Drosophil
c 389	68.6	3.0	193248	3	AC007752	AC007752 Drosophil
c 390	68.6	3.0	221239	3	AE003697	AE003697 Drosophil
c 391	68.6	3.0	246724	2	AC131807	AC131807 Rattus no
392	68.6	3.0	324288	2	AC017336	AC017336 Drosophil
393	68.2	2.9	769	6	AR497103	AR497103 Sequence
394	68.2	2.9	769	6	AR512385	AR512385 Sequence
395	68	2.9	1539	6	CQ613380	CQ613380 Sequence
396	67.8	2.9	2972	14	AF373031	AF373031 Epinotia
c 397	67.4	2.9	224097	2	AC117901	AC117901 Rattus no
c 398	67.4	2.9	251769	2	AC117913	AC117913 Rattus no
399	66.6	2.9	1793	3	AF116555	AF116555 Drosophil
400	66.4	2.9	11728	10	RATUDPGV	M74439 Rattus norv
c 401	66.4	2.9	138578	2	AC141352	AC141352 Rattus no
402	66.4	2.9	146839	2	AC142006	AC142006 Rattus no

403	66.2	2.9	1931	6	CQ609720	CQ609720	Sequence
404	66.2	2.9	1952	3	AY051629	AY051629	Drosophil
405	66	2.8	1188	6	CQ597045	CQ597045	Sequence
c 406	66	2.8	3188	6	CQ597044	CQ597044	Sequence
407	66	2.8	42006	2	AC018022	AC018022	Drosophil
c 408	66	2.8	162923	3	AC008236	AC008236	Drosophil
c 409	66	2.8	210258	3	AE003743	AE003743	Drosophil
410	65.8	2.8	1672	6	CQ598692	CQ598692	Sequence
411	65.8	2.8	1946	3	AY070939	AY070939	Drosophil
412	65.8	2.8	3751	6	CQ598691	CQ598691	Sequence
c 413	65.8	2.8	170362	3	AC009250	AC009250	Drosophil
414	65.6	2.8	179810	9	AC139345	AC139345	Papio anu
415	65.4	2.8	1488	6	CQ597786	CQ597786	Sequence
416	65.4	2.8	1584	6	CQ609723	CQ609723	Sequence
417	65.4	2.8	1920	3	AY069532	AY069532	Drosophil
418	65.4	2.8	1977	6	CQ729719	CQ729719	Sequence
419	65.4	2.8	3613	6	CQ594473	CQ594473	Sequence
420	65.4	2.8	4082	6	CQ597785	CQ597785	Sequence
421	65.4	2.8	4082	6	CQ609722	CQ609722	Sequence
422	65.4	2.8	167777	3	AC009204	AC009204	Drosophil
423	64.8	2.8	2216	10	RATUDPB	M33747 Rat UDP glu	
424	64.8	2.8	150430	10	AC133491	AC133491 Rattus no	
c 425	64.8	2.8	150430	10	AC133491	AC133491 Rattus no	
c 426	64.8	2.8	246176	2	AC114845	AC114845 Rattus no	
427	64.8	2.8	246724	2	AC131807	AC131807 Rattus no	
c 428	64.6	2.8	1369	6	AR508827	AR508827	Sequence
429	64.6	2.8	1623	6	CQ593769	CQ593769	Sequence
c 430	64.6	2.8	3683	6	CQ593768	CQ593768	Sequence
431	63.8	2.8	500	6	CQ071564	CQ071564	Sequence
432	63.8	2.8	500	6	CQ102164	CQ102164	Sequence
433	63.8	2.8	500	6	CQ141114	CQ141114	Sequence
434	63.8	2.8	500	6	CQ176767	CQ176767	Sequence
435	63.8	2.8	500	6	CQ224383	CQ224383	Sequence
436	63.8	2.8	500	6	CQ262401	CQ262401	Sequence
437	63.8	2.8	500	6	CQ336589	CQ336589	Sequence
438	63.8	2.8	689	6	BD229133	BD229133	Genotype
439	63.8	2.8	689	6	AR349385	AR349385	Sequence
440	63.8	2.8	1521	6	CQ592386	CQ592386	Sequence
441	63.8	2.8	3576	6	CQ592385	CQ592385	Sequence
c 442	63.8	2.8	27310	9	AF135416	AF135416	Homo sapi
c 443	63.8	2.8	103343	9	AC108078	AC108078	Homo sapi
c 444	63.8	2.8	138232	2	AC012582	AC012582	Homo sapi
c 445	63.8	2.8	226077	2	AC013296	AC013296	Homo sapi
446	63.6	2.7	145299	5	BX005348	BX005348	Zebrafish
447	63.6	2.7	229237	5	BX323548	BX323548	Zebrafish
448	63.6	2.7	238195	2	CR790368	CR790368	Danio rer
449	63.4	2.7	1367	9	AY529122	AY529122	Homo sapi
450	63.4	2.7	1755	3	AY071432	AY071432	Drosophil
451	63.4	2.7	21000	6	AX395166	AX395166	Sequence
c 452	63.4	2.7	132963	2	AC017518	AC017518	Drosophil
453	63.4	2.7	146309	2	CR388385	CR388385	Homo sapi
454	63.4	2.7	173723	3	AC009351	AC009351	Drosophil
455	63.4	2.7	217991	9	AC021146	AC021146	Homo sapi
456	63.4	2.7	280096	3	AE003613	AE003613	Drosophil
457	63.2	2.7	1047	6	CQ733586	CQ733586	Sequence
458	62.6	2.7	521	10	MMCGT5	U48895 Mus musculu	
459	62.6	2.7	156225	2	AC115007	AC115007	Mus muscu

460	62.6	2.7	205079	10	AC118544	AC118544 Mus muscu
461	62.6	2.7	240490	2	AC100269	AC100269 Mus muscu
462	62.4	2.7	391	6	BD237020	BD237020 Compounds
463	62.4	2.7	391	6	AR225420	AR225420 Sequence
464	62.4	2.7	391	6	AR562843	AR562843 Sequence
465	62.4	2.7	391	6	AX321490	AX321490 Sequence
466	62.2	2.7	1443	6	CQ595215	CQ595215 Sequence
467	62.2	2.7	1591	6	BD229170	BD229170 Genotype
468	62.2	2.7	1591	6	AR349422	AR349422 Sequence
c 469	62.2	2.7	3495	6	CQ595214	CQ595214 Sequence
c 470	62.2	2.7	34551	2	AC017171	AC017171 Drosophil
c 471	62.2	2.7	78938	3	AC002503	AC002503 Drosophil
472	62.2	2.7	104079	9	AC107401	AC107401 Homo sapi
473	62.2	2.7	156578	9	AC111000	AC111000 Homo sapi
c 474	62.2	2.7	174735	3	AC006402	AC006402 Drosophil
c 475	62.2	2.7	182901	3	AC093198	AC093198 Drosophil
c 476	62.2	2.7	318278	3	AE003666	AE003666 Drosophil
477	62	2.7	1543	9	AF177273	AF177273 Homo sapi
478	62	2.7	2301	10	RNU75903	U75903 Rattus norv
479	62	2.7	209071	3	AC005285	AC005285 Drosophil
480	61.8	2.7	1527	6	CQ580845	CQ580845 Sequence
481	61.8	2.7	1757	3	AY128460	AY128460 Drosophil
c 482	61.8	2.7	4647	6	CQ580844	CQ580844 Sequence
c 483	61.8	2.7	78277	2	AC020206	AC020206 Drosophil
484	61.8	2.7	81677	3	AC004377	AC004377 Drosophil
c 485	61.8	2.7	169534	3	AC008350	AC008350 Drosophil
c 486	61.8	2.7	302225	3	AE003458	AE003458 Drosophil
487	61.6	2.7	29546	3	AY246561	AY246561 Branchios
c 488	61.4	2.6	3679	6	CQ593771	CQ593771 Sequence
489	61	2.6	851	11	BV017252	BV017252 S212P6006
490	60.8	2.6	1692	8	AK109806	AK109806 Oryza sat
c 491	60.8	2.6	141545	8	OSJN00221	AL663019 Oryza sat
c 492	60.6	2.6	43323	9	AC114797	AC114797 Homo sapi
493	60.4	2.6	1500	6	CQ614607	CQ614607 Sequence
494	60	2.6	220	6	CQ080780	CQ080780 Sequence
495	60	2.6	220	6	CQ115243	CQ115243 Sequence
496	60	2.6	220	6	CQ154074	CQ154074 Sequence
497	60	2.6	220	6	CQ186655	CQ186655 Sequence
498	60	2.6	220	6	CQ237309	CQ237309 Sequence
499	60	2.6	220	6	CQ274933	CQ274933 Sequence
500	60	2.6	220	6	CQ349280	CQ349280 Sequence
501	60	2.6	402	10	MMGCGTEX4	X92126 M.musculus
502	59.6	2.6	1668	6	CQ586722	CQ586722 Sequence
503	59.6	2.6	1676	3	AY051442	AY051442 Drosophil
c 504	59.6	2.6	3740	6	CQ586721	CQ586721 Sequence
c 505	59.6	2.6	110907	14	AY229987	AY229987 Cryptophl
506	59.4	2.6	1606	6	AX675577	AX675577 Sequence
507	59.4	2.6	1606	6	AX921811	AX921811 Sequence
508	59.4	2.6	176321	2	BX942829	BX942829 Danio rer
509	59.4	2.6	186564	10	AC119816	AC119816 Mus muscu
510	59.2	2.6	427	9	HSCGT04	U31861 Human UDP-g
c 511	59	2.5	589	6	CQ225338	CQ225338 Sequence
c 512	59	2.5	589	6	CQ263337	CQ263337 Sequence
513	59	2.5	103343	9	AC108078	AC108078 Homo sapi
c 514	59	2.5	217991	9	AC021146	AC021146 Homo sapi
515	58.6	2.5	1648	8	AK064151	AK064151 Oryza sat
516	58.6	2.5	141040	8	AP004382	AP004382 Oryza sat

517	58	2.5	609	10	RATUD2A07	M35083 Rat UDP glu
518	58	2.5	1704	3	AF116554	AF116554 Drosophil
519	58	2.5	247575	2	AC125632	AC125632 Rattus no
520	57.8	2.5	2108	14	LOGVEGT	Y08294 Lacanobia o
c 521	57.8	2.5	145253	10	AC138173	AC138173 Mus muscu
c 522	57.8	2.5	186564	10	AC119816	AC119816 Mus muscu
c 523	57.4	2.5	831	6	AR524865	AR524865 Sequence
524	57.4	2.5	2036	6	CQ581913	CQ581913 Sequence
525	57.4	2.5	4386	6	CQ581912	CQ581912 Sequence
c 526	57.4	2.5	63705	9	AF135419	AF135419 sHomo sapi
527	57.4	2.5	67568	2	AC020378	AC020378 Drosophil
c 528	57.4	2.5	123406	8	AC120508	AC120508 Oryza sat
529	57.4	2.5	148977	9	AC114786	AC114786 Homo sapi
530	57.2	2.5	149712	2	AC140853	AC140853 Canis fam
c 531	57.2	2.5	149712	2	AC140853	AC140853 Canis fam
532	57.2	2.5	161844	2	AC147451	AC147451 Otolemur
c 533	57.2	2.5	208667	10	AC101835	AC101835 Mus muscu
534	57	2.5	1665	8	AB009370	AB009370 Vigna mun
535	56.8	2.4	1416	8	MZEIAGLU	L34847 Zea mays IA
536	56.8	2.4	1731	6	AR260578	AR260578 Sequence
537	56.8	2.4	161046	14	AF081810	AF081810 Lymantria
538	56.8	2.4	183755	2	AC146742	AC146742 Papio anu
c 539	56.8	2.4	183807	9	AC091778	AC091778 Papio anu
c 540	56.6	2.4	52742	2	AC147071	AC147071 Homo sapi
c 541	56.6	2.4	96776	9	AC134921	AC134921 Homo sapi
542	56.6	2.4	165501	2	AC147569	AC147569 Homo sapi
c 543	56.6	2.4	184963	9	AC147055	AC147055 Homo sapi
544	56.6	2.4	232016	2	AC148029	AC148029 Homo sapi
545	56.2	2.4	513	6	AR509041	AR509041 Sequence
546	56.2	2.4	983	6	AR284336	AR284336 Sequence
547	56.2	2.4	4966	6	CQ609719	CQ609719 Sequence
c 548	56.2	2.4	160256	2	CR753888	CR753888 Danio rer
549	56.2	2.4	183498	5	BX072578	BX072578 Zebrafish
c 550	56	2.4	183498	5	BX072578	BX072578 Zebrafish
551	55.8	2.4	350	6	AX887421	AX887421 Sequence
552	55.8	2.4	350	6	BD027031	BD027031 Sequence
c 553	55.6	2.4	106525	9	AC093720	AC093720 Homo sapi
554	55.6	2.4	147009	2	AC108490	AC108490 Homo sapi
555	55.6	2.4	153296	9	AC147070	AC147070 Homo sapi
556	55.6	2.4	155175	2	AC147064	AC147064 Homo sapi
557	55.6	2.4	181117	9	AC019173	AC019173 Homo sapi
c 558	55.4	2.4	590	11	BV100588	BV100588 RPAMSEQ0
c 559	55.2	2.4	203	6	CQ238174	CQ238174 Sequence
c 560	55.2	2.4	203	6	CQ275780	CQ275780 Sequence
561	55	2.4	1602	6	BD229242	BD229242 Genotype
562	55	2.4	1602	6	AR349494	AR349494 Sequence
563	55	2.4	106525	9	AC093720	AC093720 Homo sapi
564	54.6	2.4	848	6	CQ722622	CQ722622 Sequence
565	54.4	2.3	5122	14	AY250076	AY250076 Spodopter
566	54.4	2.3	6120	8	AF331855	AF331855 Zea mays
567	54.2	2.3	1933	9	AK130038	AK130038 Homo sapi
c 568	54.2	2.3	3642	6	CQ611789	CQ611789 Sequence
569	54	2.3	245842	2	AC106307	AC106307 Rattus no
570	53.8	2.3	138232	2	AC012582	AC012582 Homo sapi
c 571	53.8	2.3	169483	9	AC093829	AC093829 Homo sapi
572	53.8	2.3	228873	2	AC134364	AC134364 Rattus no
c 573	53.8	2.3	231284	2	AC095374	AC095374 Rattus no

574	53.6	2.3	1536	8	AB027454	AB027454 Petunia x
c 575	53.4	2.3	583	11	BV100584	BV100584 RPAMMSEQ0
c 576	53.4	2.3	583	11	BV163609	BV163609 RPAMMSEQ0
577	53.4	2.3	784	6	AX356966	AX356966 Sequence
578	53.4	2.3	784	9	HUMUGT02	M84123 Human UDP-g
579	53.4	2.3	1620	6	CQ593772	CQ593772 Sequence
580	53.4	2.3	16944	9	AY603772	AY603772 Homo sapi
c 581	53.4	2.3	23787	8	AP005917	AP005917 Oryza sat
c 582	53.4	2.3	68770	9	AC006985	AC006985 Homo sapi
c 583	53.4	2.3	176619	2	AC026497	AC026497 Homo sapi
584	53.4	2.3	198872	9	AF297093	AF297093 Homo sapi
585	53.2	2.3	1730	8	AB070746	AB070746 Vigna ang
586	53	2.3	1813	8	AY257207	AY257207 Ipomoea t
587	52.8	2.3	125020	9	AF429315	AF429315 Homo sapi
c 588	52.6	2.3	82746	1	AF453501	AF453501 Actinosyn
589	52.4	2.3	209586	2	AC148497	AC148497 Otolemur
590	52	2.2	707	6	CQ492835	CQ492835 Sequence
591	52	2.2	90972	8	AP006584	AP006584 Oryza sat
c 592	52	2.2	122193	2	AP006053	AP006053 Oryza sat
593	51.8	2.2	1584	8	AB103471	AB103471 Aralia co
c 594	51.6	2.2	576	11	BV163611	BV163611 RPAMMSEQ0
595	51.6	2.2	1594	8	AB191247	AB191247 Dianthus
596	51.6	2.2	105931	2	AC005427	AC005427 Drosophil
c 597	51.6	2.2	176321	2	BX942829	BX942829 Danio rer
598	51.4	2.2	1490	8	AY257208	AY257208 Ipomoea n
599	51.4	2.2	1786	8	AB038248	AB038248 Ipomoea b
c 600	51.4	2.2	94516	8	AP004526	AP004526 Lotus cor
601	51	2.2	1378	8	AB070743	AB070743 Vigna ang
c 602	51	2.2	1640	8	AK099344	AK099344 Oryza sat
603	51	2.2	1686	8	AK106005	AK106005 Oryza sat
604	51	2.2	1709	8	AK105785	AK105785 Oryza sat
c 605	51	2.2	1747	8	AK064324	AK064324 Oryza sat
c 606	51	2.2	1790	8	AK101518	AK101518 Oryza sat
607	51	2.2	1862	8	AK100744	AK100744 Oryza sat
608	51	2.2	124591	8	AC118347	AC118347 Oryza sat
c 609	51	2.2	146154	2	AP004400	AP004400 Oryza sat
c 610	51	2.2	156069	8	AC136842	AC136842 Oryza sat
611	51	2.2	183095	8	AP005186	AP005186 Oryza sat
612	50.8	2.2	1545	8	AB191245	AB191245 Dianthus
c 613	50.8	2.2	8596	14	AF527603	AF527603 Spodopter
c 614	50.8	2.2	38383	3	CEF35H8	Z36752 Caenorhabdi
c 615	50.8	2.2	146839	2	AC142006	AC142006 Rattus no
c 616	50.6	2.2	1105	8	AK060146	AK060146 Oryza sat
c 617	50.6	2.2	124366	8	AC131374	AC131374 Oryza sat
c 618	50.6	2.2	300029	8	AE017077	AE017077 Oryza sat
619	50.4	2.2	1391	6	CQ774188	CQ774188 Sequence
620	50.4	2.2	1494	6	AX652909	AX652909 Sequence
621	50.4	2.2	1733	8	AK106250	AK106250 Oryza sat
622	50.4	2.2	1795	8	AK066593	AK066593 Oryza sat
623	50.4	2.2	1999	6	AX756082	AX756082 Sequence
624	50.4	2.2	1999	8	AK066469	AK066469 Oryza sat
625	50.4	2.2	131616	6	CQ774045	CQ774045 Sequence
c 626	50.4	2.2	131680	14	AY522332	AY522332 Agrotis s
c 627	50.4	2.2	147472	8	AP003974	AP003974 Oryza sat
c 628	50.4	2.2	147739	8	AP005915	AP005915 Oryza sat
629	50.2	2.2	1577	8	AK107669	AK107669 Oryza sat
630	50.2	2.2	1662	8	AB070754	AB070754 Vigna ang

631	50.2	2.2	1843	8	AK065112	AK065112	Oryza sat
632	50.2	2.2	58309	8	AP006173	AP006173	Oryza sat
c 633	50.2	2.2	185449	8	AC123526	AC123526	Oryza sat
634	49.8	2.1	1086	8	AY257215	AY257215	Ipomoea a
635	49.8	2.1	6322	8	AF331854	AF331854	Zea mays
c 636	49.8	2.1	140023	4	AC093453	AC093453	Canis fam
637	49.6	2.1	563	6	CQ505416	CQ505416	Sequence
638	49.4	2.1	1578	6	E12713	E12713	Solanum mel
639	49.4	2.1	1578	8	SMGT	X77369	S.melongena
c 640	49.4	2.1	2850	14	SLPVEGT	X99073	Spodoptera
641	49.2	2.1	656	6	AX201693	AX201693	Sequence
642	49.2	2.1	657	6	AR307005	AR307005	Sequence
643	49.2	2.1	657	6	AX154755	AX154755	Sequence
644	49.2	2.1	1109	3	AY069046	AY069046	Drosophil
645	49.2	2.1	1530	6	CQ612555	CQ612555	Sequence
646	49.2	2.1	1752	6	CQ600621	CQ600621	Sequence
647	49.2	2.1	3679	6	CQ612554	CQ612554	Sequence
c 648	49.2	2.1	5189	14	SLAJ3131	AJ003131	Spodopter
649	49	2.1	501	6	CQ475453	CQ475453	Sequence
650	49	2.1	18314	3	AF125959	AF125959	Caenorhab
651	49	2.1	158826	8	AP003607	AP003607	Oryza sat
c 652	49	2.1	175667	8	AC119147	AC119147	Genomic s
c 653	49	2.1	189057	2	BX957337	BX957337	Danio rer
654	48.8	2.1	1141	6	AX083744	AX083744	Sequence
655	48.8	2.1	1496	8	AY262037	AY262037	Crocus sa
656	48.8	2.1	1689	14	LDU04321	U04321	Lymantria d
c 657	48.6	2.1	666	6	AX660993	AX660993	Sequence
658	48.6	2.1	1001	6	AR284354	AR284354	Sequence
659	48.6	2.1	1501	8	AK059016	AK059016	Oryza sat
660	48.6	2.1	1684	8	AB070755	AB070755	Vigna ang
c 661	48.6	2.1	2000	6	AX655393	AX655393	Sequence
662	48.6	2.1	2031	8	AK067710	AK067710	Oryza sat
663	48.4	2.1	789	6	AX660822	AX660822	Sequence
664	48.4	2.1	1437	6	AX505505	AX505505	Sequence
665	48.4	2.1	1455	6	AX654659	AX654659	Sequence
666	48.4	2.1	1464	8	BT015770	BT015770	Arabidops
667	48.4	2.1	1724	8	AY049277	AY049277	Arabidops
668	48.4	2.1	1727	8	AK071819	AK071819	Oryza sat
669	48.4	2.1	1781	14	MBU41999	U41999	Mamestra br
670	48.4	2.1	2396	6	E25788	E25788	Ecdysteroid
c 671	48.4	2.1	84196	8	ATT3A5	AL132979	Arabidops
c 672	48.4	2.1	89469	8	ATF18B3	AL049862	Arabidops
c 673	48.4	2.1	110086	8	AP003373	AP003373	Oryza sat
674	48.4	2.1	153656	14	AF539999	AF539999	Mamestra
675	48.4	2.1	155060	14	MBU59461	U59461	Mamestra co
676	48.2	2.1	1159	8	AY257209	AY257209	Ipomoea.p
677	48.2	2.1	1346	8	AY257206	AY257206	Ipomoea h
c 678	48.2	2.1	206924	10	AC087780	AC087780	Mus muscu
679	48	2.1	1689	8	AY087431	AY087431	Arabidops
680	48	2.1	4354	5	PPL249082	AJ249082	Pleuronec
c 681	48	2.1	130037	8	AP004192	AP004192	Oryza sat
c 682	48	2.1	139342	14	AF325155	AF325155	Spodopter
c 683	48	2.1	160215	10	AC092531	AC092531	Rattus no
684	48	2.1	164263	8	AP005515	AP005515	Oryza sat
685	48	2.1	185139	8	AP004348	AP004348	Oryza sat
c 686	48	2.1	251485	2	AC107287	AC107287	Rattus no
c 687	48	2.1	256354	10	AC120922	AC120922	Rattus no

688	47.8	2.1	1138	6	AX432482	AX432482 Sequence
689	47.8	2.1	1785	8	AK105261	AK105261 Oryza sat
690	47.8	2.1	1896	8	AK101659	AK101659 Oryza sat
691	47.8	2.1	1896	8	AK103824	AK103824 Oryza sat
692	47.8	2.1	110000	1	AE017333_08	Continuation (9 of
693	47.8	2.1	110000	1	CP000002_08	Continuation (9 of
694	47.8	2.1	146154	2	AP004400	AP004400 Oryza sat
c 695	47.8	2.1	183095	8	AP005186	AP005186 Oryza sat
696	47.6	2.1	1925	14	SLNPVEGT	X84701 Spodoptera
697	47.4	2.0	1410	6	AX653349	AX653349 Sequence
698	47.4	2.0	1729	8	AK060965	AK060965 Oryza sat
699	47.4	2.0	135323	8	CNS08CBQ	AL928753 Oryza sat
700	47.2	2.0	1609	8	AB070757	AB070757 Vigna ang
c 701	47	2.0	137678	8	AP005183	AP005183 Oryza sat
c 702	47	2.0	138653	8	AP005178	AP005178 Oryza sat
703	46.8	2.0	998	8	AJ619862	AJ619862 Arabidops
704	46.8	2.0	998	8	AJ619867	AJ619867 Arabidops
705	46.8	2.0	998	8	AJ619868	AJ619868 Arabidops
706	46.8	2.0	998	8	AJ619875	AJ619875 Arabidops
707	46.8	2.0	998	8	AJ619876	AJ619876 Arabidops
708	46.8	2.0	998	8	AJ619877	AJ619877 Arabidops
709	46.8	2.0	998	8	AJ619878	AJ619878 Arabidops
710	46.8	2.0	1000	8	AJ619869	AJ619869 Arabidops
711	46.8	2.0	1000	8	AJ619870	AJ619870 Arabidops
712	46.8	2.0	1000	8	AJ619871	AJ619871 Arabidops
713	46.8	2.0	1000	8	AJ619872	AJ619872 Arabidops
714	46.8	2.0	1000	8	AJ619873	AJ619873 Arabidops
715	46.8	2.0	1000	8	AJ619879	AJ619879 Arabidops
716	46.8	2.0	1000	8	AJ619880	AJ619880 Arabidops
717	46.8	2.0	1002	8	AJ619874	AJ619874 Arabidops
718	46.8	2.0	158482	14	AY126275	AY126275 Mamestra
719	46.6	2.0	1494	8	AF028237	AF028237 Ipomoea p
720	46.6	2.0	2531	8	ZMMC2BZ1	X13501 Maize (Bz-M
721	46.6	2.0	2919	8	ZMMCCBZ1	X13500 Zea mays (B
722	46.6	2.0	4294	8	AY191009	AY191009 Zea mays
723	46.6	2.0	5772	8	AF355378	AF355378 Zea mays
724	46.6	2.0	41355	3	U42832	U42832 Caenorhabdi
725	46.6	2.0	106186	8	AF448416	AF448416 Zea mays
726	46.6	2.0	146949	2	AL360003	AL360003 Homo sapi
727	46.6	2.0	150771	9	AL392106	AL392106 Human DNA
728	46.6	2.0	226001	8	AF391808	AF391808 Zea mays
c 729	46.6	2.0	236362	2	AC006724	AC006724 Caenorhab
730	46.4	2.0	470	11	BX322426	BX322426 Arabidops
731	46.4	2.0	1440	6	AX211632	AX211632 Sequence
c 732	46.4	2.0	1440	6	AX211634	AX211634 Sequence
733	46.4	2.0	1440	6	AX505385	AX505385 Sequence
734	46.4	2.0	1471	8	AY142676	AY142676 Arabidops
735	46.4	2.0	1599	8	AK065987	AK065987 Oryza sat
736	46.4	2.0	1615	8	AY074339	AY074339 Arabidops
737	46.4	2.0	1621	8	AY057646	AY057646 Arabidops
738	46.4	2.0	1645	8	AK105912	AK105912 Oryza sat
739	46.4	2.0	1645	8	AK119544	AK119544 Oryza sat
c 740	46.4	2.0	1657	8	AY099833	AY099833 Arabidops
741	46.4	2.0	1683	8	AK106006	AK106006 Oryza sat
742	46.4	2.0	138141	8	AP005190	AP005190 Oryza sat
c 743	46.4	2.0	168354	8	AP005185	AP005185 Oryza sat
c 744	46.4	2.0	197419	8	ATCHRIV41	AL161541 Arabidops

c 745	46.4	2.0	205065	8	ATFCA4	Z97339 Arabidopsis
c 746	46.4	2.0	250029	3	AE014820	AE014820 Plasmodiu
c 747	46.4	2.0	287560	1	AE017274	AE017274 Bacillus
748	46.2	2.0	467	11	BV008367	BV008367 MASC_STS1
c 749	46.2	2.0	490	6	CQ431226	CQ431226 Sequence
750	46.2	2.0	1458	6	AX654445	AX654445 Sequence
751	46.2	2.0	1464	6	AX653704	AX653704 Sequence
c 752	46.2	2.0	1638	8	AK105478	AK105478 Oryza sat
753	46.2	2.0	1663	8	AK062590	AK062590 Oryza sat
754	46.2	2.0	1914	8	AK068586	AK068586 Oryza sat
c 755	46.2	2.0	134534	2	AP004327	AP004327 Oryza sat
c 756	46.2	2.0	140769	8	AP003508	AP003508 Oryza sat
c 757	46.2	2.0	141036	2	AP003941	AP003941 Oryza sat
c 758	46.2	2.0	150455	8	AP004571	AP004571 Oryza sat
c 759	46.2	2.0	162520	8	AP005913	AP005913 Oryza sat
c 760	46.2	2.0	165630	8	AP003617	AP003617 Oryza sat
c 761	46.2	2.0	166005	8	AC120506	AC120506 Oryza sat
c 762	46.2	2.0	194284	5	AL954329	AL954329 Zebrafish
763	46	2.0	1259	8	MECGT6	X77463 M.esculenta
764	46	2.0	1477	6	CQ595878	CQ595878 Sequence
765	46	2.0	1553	8	AK060228	AK060228 Oryza sat
766	46	2.0	1680	8	AK069049	AK069049 Oryza sat
c 767	46	2.0	1852	8	AK105674	AK105674 Oryza sat
768	46	2.0	3528	6	CQ595877	CQ595877 Sequence
c 769	46	2.0	20493	2	AC014076	AC014076 Drosophil
c 770	46	2.0	138141	8	AP005190	AP005190 Oryza sat
771	46	2.0	148780	3	AC008326	AC008326 Drosophil
c 772	46	2.0	156983	8	OSJN00212	AL663014 Oryza sat
c 773	46	2.0	164263	8	AP005515	AP005515 Oryza sat
c 774	46	2.0	168759	8	AC079887	AC079887 Oryza sat
775	46	2.0	267997	3	AE003616	AE003616 Drosophil
776	45.8	2.0	1395	6	AX654788	AX654788 Sequence
777	45.8	2.0	1783	8	AK108674	AK108674 Oryza sat
778	45.8	2.0	5908	1	AF147704	AF147704 Streptomy
779	45.8	2.0	13511	6	AX345183	AX345183 Sequence
780	45.8	2.0	18585	6	AX281498	AX281498 Sequence
c 781	45.8	2.0	138155	2	AC151564	AC151564 Dasytus n
c 782	45.8	2.0	191765	8	AC129717	AC129717 Oryza sat
783	45.6	2.0	1510	8	AK121682	AK121682 Oryza sat
784	45.6	2.0	1639	8	AK105398	AK105398 Oryza sat
c 785	45.6	2.0	1689	8	AK063307	AK063307 Oryza sat
786	45.6	2.0	1750	8	AK119905	AK119905 Oryza sat
787	45.6	2.0	32784	3	CEF08G5	Z70682 Caenorhabdi
c 788	45.6	2.0	97352	8	AC091670	AC091670 Oryza sat
789	45.6	2.0	133889	8	AC133334	AC133334 Oryza sat
790	45.4	2.0	1688	8	AK107291	AK107291 Oryza sat
791	45.4	2.0	1706	8	AK072018	AK072018 Oryza sat
792	45.4	2.0	105227	8	AP005296	AP005296 Oryza sat
793	45.4	2.0	119926	8	AP003705	AP003705 Oryza sat
794	45.4	2.0	135611	14	AF169823	AF169823 Spodopter
795	45.4	2.0	137967	2	AC093094	AC093094 Oryza sat
c 796	45.4	2.0	165307	2	AC123749	AC123749 Mus muscu
797	45.2	1.9	994	8	AJ619855	AJ619855 Arabidops
798	45.2	1.9	994	8	AJ619856	AJ619856 Arabidops
799	45.2	1.9	1383	6	AX653292	AX653292 Sequence
800	45.2	1.9	1452	6	AX653929	AX653929 Sequence
c 801	45.2	1.9	1463	8	AK108695	AK108695 Oryza sat

802	45.2	1.9	1549	6	AX660242	AX660242 Sequence
803	45.2	1.9	1603	8	AK107156	AK107156 Oryza sat
804	45.2	1.9	1736	8	BT009372	BT009372 Triticum
805	45.2	1.9	1809	8	AK103303	AK103303 Oryza sat
806	45.2	1.9	2000	6	AX656006	AX656006 Sequence
c 807	45.2	1.9	157987	8	AP003560	AP003560 Oryza sat
808	45.2	1.9	163095	8	AP002523	AP002523 Oryza sat
809	45	1.9	45	6	AX697217	AX697217 Sequence
810	45	1.9	955	8	AB012115	AB012115 Vigna mun
811	45	1.9	1521	8	AY167672	AY167672 Zea mays
812	45	1.9	1521	8	AY167673	AY167673 Zea mays
813	45	1.9	1521	8	AY167675	AY167675 Zea mays
814	45	1.9	1521	8	AY167676	AY167676 Zea mays
815	45	1.9	1521	8	AY167679	AY167679 Zea mays
816	45	1.9	1536	6	E49073	E49073 UDP-D-Gluco
817	45	1.9	1561	8	AB191249	AB191249 Dianthus
818	45	1.9	1575	8	AB002818	AB002818 Perilla f
819	45	1.9	1594	8	ZMW22BZ1	X13502 Maize (Bz-W
820	45	1.9	1732	6	E49068	E49068 UDP-D-Gluco
821	45	1.9	1732	8	AB033758	AB033758 Citrus un
822	45	1.9	2908	8	ZMBZW22	X07937 Maize Bz-W2
823	45	1.9	3181	8	ZMBZR	X07941 Maize bronz
c 824	45	1.9	37329	3	U97009	U97009 Caenorhabdi
825	45	1.9	103960	8	ATAC011664	AC011664 Arabidops
826	45	1.9	147472	8	AP003974	AP003974 Oryza sat
c 827	45	1.9	149227	2	AC146976	AC146976 Zea mays
c 828	45	1.9	179810	9	AC139345	AC139345 Papio anu
c 829	45	1.9	288479	2	AC146814	AC146814 Zea mays
c 830	44.8	1.9	774	6	BD019848	BD019848 Novel gen
c 831	44.8	1.9	774	6	BD099786	BD099786 Novel gen
832	44.8	1.9	858	10	RATUGT1B3G	D38067 Rattus norv
833	44.8	1.9	995	8	AJ619882	AJ619882 Arabidops
834	44.8	1.9	995	8	AJ619883	AJ619883 Arabidops
835	44.8	1.9	1362	6	AX412617	AX412617 Sequence
836	44.8	1.9	1362	6	AX507722	AX507722 Sequence
837	44.8	1.9	1362	6	AX589823	AX589823 Sequence
838	44.8	1.9	1362	6	AX652007	AX652007 Sequence
839	44.8	1.9	1521	8	AK110892	AK110892 Oryza sat
840	44.8	1.9	1787	8	AF303396	AF303396 Phaseolus
c 841	44.8	1.9	78089	3	AC024876	AC024876 Caenorhab
c 842	44.8	1.9	95824	9	AC068888	AC068888 Homo sapi
c 843	44.8	1.9	103223	8	AC007153	AC007153 Arabidops
844	44.8	1.9	110000	2	AC109940_0	AC109940 Rattus no
845	44.8	1.9	192969	2	AC150463	AC150463 Callithri
846	44.8	1.9	221618	10	AC092530	AC092530 Rattus no
c 847	44.8	1.9	224007	2	AC111764	AC111764 Rattus no
c 848	44.8	1.9	298804	2	AC006911	AC006911 Caenorhab
849	44.8	1.9	299081	2	AC006892	AC006892 Caenorhab
850	44.6	1.9	762	6	BD224494	BD224494 Materials
851	44.6	1.9	762	6	AR216544	AR216544 Sequence
c 852	44.6	1.9	1141	6	AX083744	AX083744 Sequence
853	44.6	1.9	1558	8	AB070748	AB070748 Vigna ang
854	44.6	1.9	1662	8	AK064105	AK064105 Oryza sat
855	44.6	1.9	2591	8	AK106639	AK106639 Oryza sat
856	44.6	1.9	110000	1	AE017263_2	Continuation (3 of
c 857	44.6	1.9	159861	8	AP005012	AP005012 Oryza sat
858	44.6	1.9	287476	1	AE017271	AE017271 Bacillus

	859	44.4	1.9	1175	8	AB074489	AB074489	Malus x d
	860	44.4	1.9	54025	8	AP006525	AP006525	Oryza sat
	861	44.2	1.9	1666	8	AK106038	AK106038	Oryza sat
c	862	44.2	1.9	133427	2	AC134521	AC134521	Medicago
c	863	44.2	1.9	144271	8	AC098682	AC098682	Genomic s
	864	44.2	1.9	302524	8	AE017075	AE017075	Oryza sat
	865	44	1.9	1895	8	AK108846	AK108846	Oryza sat
	866	44	1.9	3986	8	AY490797	AY490797	Helianthu
	867	44	1.9	4556	9	AF153832S3	AF153834	Homo sapi
c	868	44	1.9	144392	9	HS67K17	AL023584	Human DNA
	869	44	1.9	148762	8	AP002843	AP002843	Oryza sat
c	870	44	1.9	172752	2	AC116496	AC116496	Mus muscu
	871	44	1.9	236164	2	AC113057	AC113057	Mus muscu
	872	43.8	1.9	432	6	A63526	A63526	Sequence 7
	873	43.8	1.9	1152	6	AX653506	AX653506	Sequence
	874	43.8	1.9	1482	6	AX653177	AX653177	Sequence
	875	43.8	1.9	1654	8	AK121725	AK121725	Oryza sat
	876	43.8	1.9	1660	8	AB070745	AB070745	Vigna ang
	877	43.8	1.9	1726	8	AK064395	AK064395	Oryza sat
	878	43.8	1.9	1798	8	AY663785	AY663785	Fragaria
	879	43.8	1.9	1958	8	AY171598	AY171598	Fragaria
	880	43.8	1.9	37845	3	CEF01D4	Z81054	Caenorhabdi
c	881	43.8	1.9	46394	3	CBRG17D06	AC084511	Caenorhab
	882	43.8	1.9	134534	2	AP004327	AP004327	Oryza sat
	883	43.8	1.9	141036	2	AP003941	AP003941	Oryza sat
	884	43.8	1.9	165630	8	AP003617	AP003617	Oryza sat
c	885	43.8	1.9	182870	3	AC116960	AC116960	Dictyoste
	886	43.8	1.9	184645	2	AC108395	AC108395	Mus muscu
	887	43.8	1.9	349954	6	AX196297	AX196297	Sequence
	888	43.6	1.9	617	12	AY199453	AY199453	Arabidops
	889	43.6	1.9	993	8	AJ619881	AJ619881	Arabidops
	890	43.6	1.9	993	8	AJ619884	AJ619884	Arabidops
	891	43.6	1.9	993	8	AJ619885	AJ619885	Arabidops
	892	43.6	1.9	994	8	AJ619857	AJ619857	Arabidops
	893	43.6	1.9	994	8	AJ619858	AJ619858	Arabidops
	894	43.6	1.9	994	8	AJ619859	AJ619859	Arabidops
	895	43.6	1.9	994	8	AJ619860	AJ619860	Arabidops
	896	43.6	1.9	994	8	AJ619861	AJ619861	Arabidops
	897	43.6	1.9	994	8	AJ619863	AJ619863	Arabidops
	898	43.6	1.9	994	8	AJ619864	AJ619864	Arabidops
	899	43.6	1.9	994	8	AJ619865	AJ619865	Arabidops
	900	43.6	1.9	994	8	AJ619866	AJ619866	Arabidops
	901	43.6	1.9	1001	6	AR284363	AR284363	Sequence
	902	43.6	1.9	1001	6	AR284364	AR284364	Sequence
	903	43.6	1.9	1001	6	AR284365	AR284365	Sequence
	904	43.6	1.9	1001	6	AR284367	AR284367	Sequence
	905	43.6	1.9	1021	6	BD229240	BD229240	Genotype
	906	43.6	1.9	1021	6	AR349492	AR349492	Sequence
	907	43.6	1.9	1073	8	MECGT2	X77461	M.esculenta
	908	43.6	1.9	1350	6	AX412670	AX412670	Sequence
	909	43.6	1.9	1350	6	AX507107	AX507107	Sequence
	910	43.6	1.9	1350	6	AX651538	AX651538	Sequence
	911	43.6	1.9	1350	8	BT010327	BT010327	Arabidops
	912	43.6	1.9	1437	6	CQ759478	CQ759478	Sequence
	913	43.6	1.9	1437	6	AX211615	AX211615	Sequence
	914	43.6	1.9	1527	8	AY087340	AY087340	Arabidops
	915	43.6	1.9	1565	8	AY087866	AY087866	Arabidops

	916	43.6	1.9	1582	8	AY062483	AY062483 Arabidops
c	917	43.6	1.9	98734	8	AC002333	AC002333 Arabidops
	918	43.6	1.9	103785	8	ATF1I16	AL161667 Arabidops
	919	43.6	1.9	110036	8	AC142095	AC142095 Medicago
c	920	43.6	1.9	203301	2	AC147067	AC147067 Homo sapi
	921	43.4	1.9	929	8	AK059765	AK059765 Oryza sat
	922	43.4	1.9	1359	6	AX654630	AX654630 Sequence
	923	43.4	1.9	1521	8	AY167674	AY167674 Zea mays
	924	43.4	1.9	1521	8	AY167677	AY167677 Zea mays
	925	43.4	1.9	1521	8	AY167678	AY167678 Zea mays
	926	43.4	1.9	1604	8	AK106312	AK106312 Oryza sat
	927	43.4	1.9	1621	8	AK100189	AK100189 Oryza sat
	928	43.4	1.9	4296	8	AK068604	AK068604 Oryza sat
	929	43.4	1.9	8867	8	AY191010	AY191010 Zea mays
	930	43.4	1.9	114283	2	AC149822	AC149822 Zea mays
	931	43.4	1.9	148191	8	OSJN00067	AL606602 Oryza sat
	932	43.4	1.9	149049	8	AP004340	AP004340 Oryza sat
c	933	43.4	1.9	157452	2	AC087800	AC087800 Mus muscu
	934	43.4	1.9	163032	8	AP004263	AP004263 Oryza sat
	935	43.2	1.9	1001	6	AR284366	AR284366 Sequence
	936	43.2	1.9	1546	8	AK068362	AK068362 Oryza sat
	937	43.2	1.9	10329	6	AX347024	AX347024 Sequence
c	938	43.2	1.9	43154	3	U55369	U55369 Caenorhabdi
c	939	43.2	1.9	103234	2	AP003997	AP003997 Oryza sat
c	940	43.2	1.9	128955	8	AP003754	AP003754 Oryza sat
c	941	43.2	1.9	141040	8	AP004382	AP004382 Oryza sat
c	942	43.2	1.9	146951	8	AP003270	AP003270 Oryza sat
c	943	43.2	1.9	157248	8	AP004300	AP004300 Oryza sat
	944	43.2	1.9	226077	2	AC013296	AC013296 Homo sapi
	945	43.2	1.9	229569	2	AC107424	AC107424 Homo sapi
c	946	43.2	1.9	251131	2	AC111217	AC111217 Rattus no
	947	43.2	1.9	349980	6	AX344569	AX344569 Sequence
	948	43.2	1.9	349980	6	AX344570	AX344570 Sequence
	949	43.2	1.9	349980	6	AX344573	AX344573 Sequence
	950	43.2	1.9	349980	6	AX344574	AX344574 Sequence
c	951	43	1.9	340	8	AY027263	AY027263 Arabidops
	952	43	1.9	393	6	AX660985	AX660985 Sequence
c	953	43	1.9	469	11	BV009002	BV009002 MASC_STS1
c	954	43	1.9	519	11	BV008995	BV008995 MASC_STS1
	955	43	1.9	1350	6	CQ759477	CQ759477 Sequence
	956	43	1.9	1440	8	AF190634	AF190634 Nicotiana
	957	43	1.9	110000	1	AE017180_09	Continuation (10 o
	958	43	1.9	142376	8	AF503433	AF503433 Sorghum b
	959	42.8	1.8	1476	6	AX653505	AX653505 Sequence
	960	42.8	1.8	1597	8	AK068878	AK068878 Oryza sat
	961	42.8	1.8	1637	14	AF313417	AF313417 Anticarsi
	962	42.8	1.8	1819	8	AF117267	AF117267 Malus dom
c	963	42.8	1.8	35033	3	AF067615	AF067615 Caenorhab
c	964	42.8	1.8	100999	14	AF270937	AF270937 Plutella
c	965	42.8	1.8	124526	8	AC146585	AC146585 Medicago
	966	42.8	1.8	131689	9	AC010588	AC010588 Homo sapi
	967	42.8	1.8	161658	9	AC008505	AC008505 Homo sapi
c	968	42.8	1.8	168753	9	AC006120	AC006120 Homo sapi
c	969	42.8	1.8	276829	2	AC006741	AC006741 Caenorhab
	970	42.6	1.8	432	5	PFL291986	AJ291986 Platichth
	971	42.6	1.8	1368	6	AX766275	AX766275 Sequence
	972	42.6	1.8	1760	8	AK099049	AK099049 Oryza sat

973	42.6	1.8	1761	8	AK066462	AK066462 Oryza sat
974	42.6	1.8	2025	6	AR152488	AR152488 Sequence
975	42.6	1.8	2025	6	BD005789	BD005789 Biologica
976	42.6	1.8	2025	14	HZU89958	U89958 Helicoverpa
977	42.6	1.8	2505	14	AF503939	AF503939 Helicover
978	42.6	1.8	27908	3	CET04H1	Z78200 Caenorhabdi
979	42.6	1.8	31495	14	AF275264	AF275264 Helicover
c 980	42.6	1.8	84203	8	AC005106	AC005106 Genomic s
c 981	42.6	1.8	87577	2	BX640459	BX640459 Danio rer
982	42.6	1.8	114078	2	BX640498	BX640498 Danio rer
c 983	42.6	1.8	121889	5	BX255952	BX255952 Zebrafish
c 984	42.6	1.8	122128	8	CNS07YPV	AL731761 Oryza sat
985	42.6	1.8	130759	14	AF303045	AF303045 Helicover
986	42.6	1.8	130869	14	AF334030	AF334030 Helicover
987	42.6	1.8	131403	14	AF271059	AF271059 Helicove
c 988	42.6	1.8	158158	8	AC146522	AC146522 Oryza sat
989	42.6	1.8	195190	2	AC110843	AC110843 Rattus no
c 990	42.6	1.8	246998	2	CR450707	CR450707 Danio rer
991	42.6	1.8	250621	2	CR792433	CR792433 Danio rer
992	42.4	1.8	121	6	AX266625	AX266625 Sequence
c 993	42.4	1.8	121	6	AX266626	AX266626 Sequence
994	42.4	1.8	1410	6	AX211623	AX211623 Sequence
c 995	42.4	1.8	1410	6	AX211625	AX211625 Sequence
996	42.4	1.8	1410	6	AX720222	AX720222 Sequence
997	42.4	1.8	1410	6	AX766274	AX766274 Sequence
998	42.4	1.8	1410	8	AY078051	AY078051 Arabidops
999	42.4	1.8	1428	6	AX507686	AX507686 Sequence
1000	42.4	1.8	1428	8	BT012573	BT012573 Arabidops
1001	42.4	1.8	1430	6	AX211635	AX211635 Sequence
c1002	42.4	1.8	1430	6	AX211637	AX211637 Sequence
1003	42.4	1.8	1437	8	AY663786	AY663786 Fragaria
1004	42.4	1.8	1560	6	AX412846	AX412846 Sequence
1005	42.4	1.8	1563	6	AX654346	AX654346 Sequence
1006	42.4	1.8	1592	8	AF196777	AF196777 Arabidops
1007	42.4	1.8	1597	8	AF367358	AF367358 Arabidops
1008	42.4	1.8	1705	8	AK099145	AK099145 Oryza sat
1009	42.4	1.8	1719	8	AK070110	AK070110 Oryza sat
1010	42.4	1.8	1776	8	AK059031	AK059031 Oryza sat
1011	42.4	1.8	2000	6	AX655393	AX655393 Sequence
1012	42.4	1.8	91841	10	AL606971	AL606971 Mouse DNA
c1013	42.4	1.8	126497	9	AC019044	AC019044 Homo sapi
c1014	42.4	1.8	130779	8	OSJN00283	AL731638 Oryza sat
c1015	42.4	1.8	141883	8	OSJN00271	AL731626 Oryza sat
c1016	42.4	1.8	148191	8	OSJN00067	AL606602 Oryza sat
c1017	42.4	1.8	156649	8	AC144738	AC144738 Oryza sat
c1018	42.4	1.8	157648	2	BX901886	BX901886 Danio rer
c1019	42.4	1.8	164896	2	CR762432	CR762432 Danio rer
1020	42.4	1.8	168759	8	AC079887	AC079887 Oryza sat
1021	42.4	1.8	180557	9	AC007250	AC007250 Homo sapi
c1022	42.4	1.8	197061	10	AL606914	AL606914 Mouse DNA
1023	42.4	1.8	301450	1	AP003185	AP003185 Clostridi
c1024	42.2	1.8	708	5	AF352753	AF352753 Oncorhync
1025	42.2	1.8	1734	8	AK060513	AK060513 Oryza sat
1026	42.2	1.8	2438	8	AF426026	AF426026 Piromyces
1027	42.2	1.8	11319	1	AE010792	AE010792 Methanosa
1028	42.2	1.8	40862	6	AX346975	AX346975 Sequence
1029	42.2	1.8	70746	2	AC150844	AC150844 Medicago

c1030	42.2	1.8	75840	8	AF527807	AF527807 Sorghum b
1031	42.2	1.8	117124	8	AP006360	AP006360 Lotus cor
c1032	42.2	1.8	165501	2	AC147569	AC147569 Homo sapi
1033	42.2	1.8	191821	9	AC022616	AC022616 Homo sapi
1034	42	1.8	408	6	AR496501	AR496501 Sequence
1035	42	1.8	408	6	AR511783	AR511783 Sequence
1036	42	1.8	1521	14	AY048771	AY048771 Bombyx mo
1037	42	1.8	1800	6	AR362648	AR362648 Sequence
1038	42	1.8	2793	6	AR027919	AR027919 Sequence
1039	42	1.8	2793	6	I63351	I63351 Sequence 5
1040	42	1.8	2793	14	NPHEGT	M22619 Autographa
1041	42	1.8	14613	14	NPHCUECDYS	M96361 Autographa
c1042	42	1.8	40324	6	AX458634	AX458634 Sequence
1043	42	1.8	50000	6	BD187788	BD187788 A virus i
c1044	42	1.8	67884	2	AC115103	AC115103 Homo sapi
1045	42	1.8	117951	9	AC023049	AC023049 Homo sapi
c1046	42	1.8	119217	14	AF499596	AF499596 Phthorima
1047	42	1.8	128413	14	NPHT3COMP	L33180 Bombyx mori
1048	42	1.8	133894	6	A48542	A48542 Sequence 1
1049	42	1.8	133894	14	L22858	L22858 Autographa
1050	42	1.8	149955	14	AY077832	AY077832 Sheeppox
1051	42	1.8	150158	8	AC136905	AC136905 Oryza sat
1052	42	1.8	154298	8	AP003504	AP003504 Oryza sat
1053	42	1.8	156514	8	AP003514	AP003514 Oryza sat
1054	42	1.8	174183	2	AC149689	AC149689 Bos tauru
1055	42	1.8	174500	8	AP004738	AP004738 Oryza sat
1056	42	1.8	182726	2	AC084436	AC084436 Homo sapi
1057	42	1.8	185592	10	AL773522	AL773522 Mouse DNA
1058	42	1.8	320135	2	AC151850	AC151850 Takifugu
c1059	41.8	1.8	424	6	AR495496	AR495496 Sequence
c1060	41.8	1.8	424	6	AR510778	AR510778 Sequence
1061	41.8	1.8	1218	6	CQ801246	CQ801246 Sequence
1062	41.8	1.8	1457	8	AF127218	AF127218 Forsythia
1063	41.8	1.8	1470	6	CQ804574	CQ804574 Sequence
1064	41.8	1.8	1470	8	BT008765	BT008765 Arabidops
1065	41.8	1.8	1605	8	AY081339	AY081339 Arabidops
1066	41.8	1.8	2043	8	AB013598	AB013598 Verbena h
1067	41.8	1.8	2326	8	HVBRNZ1H	X15694 Barley bron
1068	41.8	1.8	6174	6	CQ801273	CQ801273 Sequence
1069	41.8	1.8	10325	6	CQ801245	CQ801245 Sequence
1070	41.8	1.8	12134	6	CQ801279	CQ801279 Sequence
c1071	41.8	1.8	50436	9	AL391258	AL391258 Human DNA
1072	41.8	1.8	57121	2	AC084255	AC084255 Homo sapi
1073	41.8	1.8	82139	3	AC115684	AC115684 Dictyoste
c1074	41.8	1.8	97681	9	AL138931	AL138931 Human DNA
1075	41.8	1.8	107200	8	AC006551	AC006551 Arabidops
1076	41.8	1.8	109873	8	AP003872	AP003872 Oryza sat
c1077	41.8	1.8	115248	5	BX255908	BX255908 Zebrafish
c1078	41.8	1.8	131158	14	AY327402	AY327402 Choriston
1079	41.8	1.8	148544	8	AP004636	AP004636 Oryza sat
c1080	41.8	1.8	177320	2	AL356777	AL356777 Homo sapi
c1081	41.8	1.8	192867	9	AL358815	AL358815 Human DNA
1082	41.8	1.8	194693	2	CR753837	CR753837 Danio rer
c1083	41.8	1.8	233688	2	BX571949	BX571949 Danio rer
1084	41.6	1.8	466	6	AR495991	AR495991 Sequence
1085	41.6	1.8	466	6	AR511273	AR511273 Sequence
1086	41.6	1.8	700	8	AY201033	AY201033 Arabidops

1087	41.6	1.8	1323	6	AX653753	AX653753 Sequence
1088	41.6	1.8	1480	8	AK118988	AK118988 Arabidops
1089	41.6	1.8	7238	6	AX345350	AX345350 Sequence
1090	41.6	1.8	103517	8	AC073395	AC073395 Arabidops
1091	41.6	1.8	117296	8	AC008153	AC008153 Arabidops
1092	41.6	1.8	125283	8	AC144345	AC144345 Medicago
c1093	41.6	1.8	125623	3	AC115599	AC115599 Dictyoste
1094	41.6	1.8	167628	9	AC092570	AC092570 Homo sapi
c1095	41.6	1.8	197679	10	AC087801	AC087801 Mus muscu
1096	41.6	1.8	207945	10	AC123945	AC123945 Mus muscu
1097	41.6	1.8	211456	10	AL928926	AL928926 Mouse DNA
c1098	41.6	1.8	219293	2	AC141471	AC141471 Mus muscu
1099	41.4	1.8	281	8	NTA538414	AJ538414 Nicotiana
1100	41.4	1.8	468	11	BV008994	BV008994 MASC_STSl
1101	41.4	1.8	525	11	BV009008	BV009008 MASC_STSl
1102	41.4	1.8	1381	8	BT005494	BT005494 Arabidops
1103	41.4	1.8	1434	6	AX211619	AX211619 Sequence
1104	41.4	1.8	1507	8	AY084687	AY084687 Arabidops
1105	41.4	1.8	1584	8	AK071127	AK071127 Oryza sat
1106	41.4	1.8	1618	8	BT004159	BT004159 Arabidops
1107	41.4	1.8	37329	3	U97009	U97009 Caenorhabdi
1108	41.4	1.8	38951	3	CEAC3	Z71177 Caenorhabdi
1109	41.4	1.8	45701	9	AC099412	AC099412 Homo sapi
1110	41.4	1.8	45868	8	AC145456	AC145456 Cicer ari
c1111	41.4	1.8	75125	8	AB025604	AB025604 Arabidops
1112	41.4	1.8	138870	8	AP005659	AP005659 Oryza sat
1113	41.4	1.8	145988	2	AC024059	AC024059 Homo sapi
c1114	41.4	1.8	161586	9	AC090179	AC090179 Homo sapi
c1115	41.4	1.8	181991	2	AC068322	AC068322 Homo sapi
1116	41.4	1.8	195806	9	AC027243	AC027243 Homo sapi
c1117	41.4	1.8	215251	2	AC105505	AC105505 Rattus no
1118	41.4	1.8	236880	2	AC125831	AC125831 Rattus no
1119	41.4	1.8	248489	2	AC095253	AC095253 Rattus no
1120	41.2	1.8	1374	6	CQ805414	CQ805414 Sequence
1121	41.2	1.8	1374	6	AX506881	AX506881 Sequence
1122	41.2	1.8	1374	6	AX651852	AX651852 Sequence
1123	41.2	1.8	1405	8	AY117218	AY117218 Arabidops
1124	41.2	1.8	1617	8	AY056277	AY056277 Arabidops
1125	41.2	1.8	1732	8	AK099055	AK099055 Oryza sat
1126	41.2	1.8	1785	8	AK071953	AK071953 Oryza sat
1127	41.2	1.8	4686	6	AX654735	AX654735 Sequence
1128	41.2	1.8	7829	6	AX251889	AX251889 Sequence
1129	41.2	1.8	7829	6	AX344283	AX344283 Sequence
1130	41.2	1.8	7829	6	AX346007	AX346007 Sequence
1131	41.2	1.8	7829	6	AX348698	AX348698 Sequence
1132	41.2	1.8	10710	6	AX345795	AX345795 Sequence
c1133	41.2	1.8	14284	14	AF439352	AF439352 Choriston
1134	41.2	1.8	24768	3	CET07C5	Z50006 Caenorhabdi
c1135	41.2	1.8	100665	8	AC006533	AC006533 Arabidops
c1136	41.2	1.8	112065	8	AC109596	AC109596 Oryza sat
c1137	41.2	1.8	124131	2	AC016335	AC016335 Homo sapi
1138	41.2	1.8	128755	9	AC013587	AC013587 Homo sapi
1139	41.2	1.8	129564	9	AC087302	AC087302 Homo sapi
c1140	41.2	1.8	133352	8	AC108499	AC108499 Oryza sat
c1141	41.2	1.8	138717	10	AL929416	AL929416 Mouse DNA
1142	41.2	1.8	159891	8	AP004864	AP004864 Oryza sat
1143	41.2	1.8	161624	2	AP001493	AP001493 Homo sapi

c1144	41.2	1.8	167580	2	AC146124	AC146124	Pan trogl
c1145	41.2	1.8	167932	2	AC068133	AC068133	Homo sapi
c1146	41.2	1.8	170270	2	AP001548	AP001548	Homo sapi
1147	41.2	1.8	170413	2	AC090405	AC090405	Homo sapi
c1148	41.2	1.8	172655	2	AC104203	AC104203	Mus muscu
c1149	41.2	1.8	174463	5	BX511007	BX511007	Zebrafish
1150	41.2	1.8	174645	9	AC091111	AC091111	Homo sapi
1151	41.2	1.8	175850	2	AP001399	AP001399	Homo sapi
1152	41.2	1.8	180915	8	GTAJ10592	AJ010592	Guillard
1153	41.2	1.8	186150	2	AP001544	AP001544	Homo sapi
1154	41.2	1.8	188800	2	AC015846	AC015846	Homo sapi
c1155	41.2	1.8	194487	2	AP002896	AP002896	Homo sapi
c1156	41.2	1.8	202699	2	BS000628	BS000628	Pan trogl
c1157	41.2	1.8	204120	8	AY661659	AY661659	Sorghum b
1158	41.2	1.8	204340	9	AC091103	AC091103	Homo sapi
1159	41.2	1.8	209710	9	CNS01DXF	AL139296	Human chr
1160	41.2	1.8	230714	9	AC147345	AC147345	Pan trogl
1161	41.2	1.8	271793	2	BX572620	BX572620	Danio rer
c1162	41.2	1.8	291421	2	AC132939	AC132939	Mus muscu
1163	41	1.8	1423	8	AY519364	AY519364	Citrus si
1164	41	1.8	1479	6	AX653930	AX653930	Sequence
1165	41	1.8	2000	6	AX656007	AX656007	Sequence
1166	41	1.8	2111	14	AF000009	AF000009	Heliothis
c1167	41	1.8	110000	2	CR388160_1	Continuation (2 of	
c1168	41	1.8	135507	9	AL590733	AL590733	Human DNA
1169	41	1.8	146885	2	BX957322	BX957322	Danio rer
1170	41	1.8	159419	5	AC144823	AC144823	Danio rer
c1171	41	1.8	162134	2	AC022478	AC022478	Homo sapi
1172	41	1.8	172614	9	AL929302	AL929302	Human DNA
1173	41	1.8	173411	9	AC092754	AC092754	Homo sapi
1174	41	1.8	176202	9	CNS05TF3	AL359951	Human chr
1175	41	1.8	187429	9	AC092755	AC092755	Homo sapi
c1176	41	1.8	208770	2	CR388155	CR388155	Danio rer
1177	41	1.8	216567	2	BX927074	BX927074	Danio rer
1178	41	1.8	229637	2	CR556716	CR556716	Danio rer
1179	40.8	1.8	1361	8	AB070749	AB070749	Vigna ang
1180	40.8	1.8	1398	6	AX653340	AX653340	Sequence
1181	40.8	1.8	1415	8	MECGT1	X77459	M.esculenta
c1182	40.8	1.8	1581	8	AK120020	AK120020	Oryza sat
1183	40.8	1.8	1586	8	AK064270	AK064270	Oryza sat
1184	40.8	1.8	1656	8	AK068040	AK068040	Oryza sat
c1185	40.8	1.8	1706	8	AK108055	AK108055	Oryza sat
1186	40.8	1.8	1962	8	AK063325	AK063325	Oryza sat
c1187	40.8	1.8	7554	3	AY160096	AY160096	Dictyoste
c1188	40.8	1.8	16841	9	AB044136	AB044136	Homo sapi
1189	40.8	1.8	36846	2	AC149390	AC149390	Phakopsor
c1190	40.8	1.8	59940	2	AC024414	AC024414	Homo sapi
1191	40.8	1.8	70204	9	AC010737	AC010737	Homo sapi
1192	40.8	1.8	77204	8	AB046438	AB046438	Arabidops
c1193	40.8	1.8	84705	3	CEY48E1B	Z93393	Caenorhabdi
1194	40.8	1.8	97352	8	AC091670	AC091670	Oryza sat
1195	40.8	1.8	102230	8	AP004045	AP004045	Oryza sat
c1196	40.8	1.8	121501	8	AC069557	AC069557	Genomic S
1197	40.8	1.8	132558	3	AC025716	AC025716	Caenorhab
c1198	40.8	1.8	133476	9	AC008804	AC008804	Homo sapi
c1199	40.8	1.8	133889	8	AC133334	AC133334	Oryza sat
c1200	40.8	1.8	149972	2	AC101817	AC101817	Mus muscu

1201	40.8	1.8	153297	2	AC027558	AC027558 Homo sapi
1202	40.8	1.8	178376	8	AP005008	AP005008 Oryza sat
c1203	40.8	1.8	190666	2	AY245865	AY245865 Homo sapi
1204	40.8	1.8	198845	5	BX510333	BX510333 Zebrafish
1205	40.8	1.8	203595	2	CR385054	CR385054 Danio rer
1206	40.8	1.8	247275	10	AC100736	AC100736 Mus muscu
c1207	40.8	1.8	274626	2	AC006903	AC006903 Caenorhab
1208	40.8	1.8	340801	2	AC006751	AC006751 Caenorhab
c1209	40.8	1.8	348174	3	CR382399	CR382399 Plasmodiu
c1210	40.8	1.8	349960	6	AX573241	AX573241 Sequence
1211	40.6	1.8	1768	8	AB098614	AB098614 Glycyrrhi
1212	40.6	1.8	6325	3	DDI012088	AJ012088 Dictyoste
1213	40.6	1.8	38206	9	AL356984	AL356984 Human DNA
c1214	40.6	1.8	110000	2	PFMAL13_04	Continuation (5 of
c1215	40.6	1.8	143291	9	HS163G9	AL008733 Human DNA
c1216	40.6	1.8	173223	9	AP003777	AP003777 Homo sapi
1217	40.6	1.8	214480	2	AC113517	AC113517 Mus muscu
1218	40.6	1.8	222186	2	AC120362	AC120362 Mus muscu
1219	40.6	1.8	257258	2	AC105322	AC105322 Mus muscu
1220	40.6	1.8	293431	2	PFMAL13P4	AL049181 Plasmodiu
1221	40.6	1.8	349980	6	AX344551	AX344551 Sequence
1222	40.4	1.7	404	3	MAU42338	U42338 Meloidogyne
1223	40.4	1.7	1293	8	BT011794	BT011794 Arabidops
1224	40.4	1.7	1437	6	AX652925	AX652925 Sequence
1225	40.4	1.7	1440	6	AX766278	AX766278 Sequence
1226	40.4	1.7	1514	8	AK110876	AK110876 Oryza sat
1227	40.4	1.7	1537	8	CAR400861	AJ400861 Cicer ari
1228	40.4	1.7	1567	8	AY625694	AY625694 Oryza sat
1229	40.4	1.7	1664	8	AK061830	AK061830 Oryza sat
1230	40.4	1.7	1686	8	AK102335	AK102335 Oryza sat
1231	40.4	1.7	1725	8	AK064351	AK064351 Oryza sat
1232	40.4	1.7	1779	8	AK102415	AK102415 Oryza sat
c1233	40.4	1.7	59793	8	AB025634	AB025634 Arabidops
1234	40.4	1.7	110000	2	PFMAL8P1_11	Continuation (12 o
1235	40.4	1.7	132254	3	AC116330	AC116330 Dictyoste
1236	40.4	1.7	157987	8	AP003560	AP003560 Oryza sat
1237	40.4	1.7	211799	2	AC138229	AC138229 Mus muscu
1238	40.4	1.7	226627	2	AC134181	AC134181 Rattus no
c1239	40.4	1.7	230926	2	AC114457	AC114457 Rattus no
1240	40.4	1.7	348034	3	CR382400	CR382400 Plasmodiu
c1241	40.2	1.7	366	1	AY430162	AY430162 Helicobac
c1242	40.2	1.7	366	1	AY430163	AY430163 Helicobac
c1243	40.2	1.7	366	1	AY430165	AY430165 Helicobac
c1244	40.2	1.7	805	11	BV026811	BV026811 S212P6802
1245	40.2	1.7	863	8	HVU496572	AJ496572 Hordeum v
1246	40.2	1.7	1383	6	CQ806198	CQ806198 Sequence
1247	40.2	1.7	1399	8	AY128739	AY128739 Arabidops
1248	40.2	1.7	1402	8	AY133752	AY133752 Arabidops
1249	40.2	1.7	1418	8	AY114654	AY114654 Arabidops
1250	40.2	1.7	1426	8	AY072325	AY072325 Arabidops
1251	40.2	1.7	1492	8	AY062589	AY062589 Arabidops
1252	40.2	1.7	1565	8	AY074526	AY074526 Arabidops
1253	40.2	1.7	1640	8	AK105783	AK105783 Oryza sat
1254	40.2	1.7	1665	8	AK105966	AK105966 Oryza sat
1255	40.2	1.7	1673	8	AK119530	AK119530 Oryza sat
1256	40.2	1.7	36075	3	AF025468	AF025468 Caenorhab
c1257	40.2	1.7	96123	9	AC114311	AC114311 Homo sapi

c1258	40.2	1.7	98101	8	ATF2K13	AL391141	Arabidops
1259	40.2	1.7	104305	8	AC140022	AC140022	Medicago
1260	40.2	1.7	107014	8	OSJN00218	AL663021	Oryza sat
c1261	40.2	1.7	107014	8	OSJN00218	AL663021	Oryza sat
1262	40.2	1.7	108530	5	BX247884	BX247884	Zebrafish
1263	40.2	1.7	109918	9	AC114279	AC114279	Homo sapi
c1264	40.2	1.7	110000	2	AC115142_0	AC115142	Rattus no
c1265	40.2	1.7	123500	14	U53466	U53466	Cydia pomon
c1266	40.2	1.7	129563	8	OSJN00008	AL606443	Oryza sat
c1267	40.2	1.7	140691	9	AF159056	AF159056	Homo sapi
1268	40.2	1.7	143036	2	AC015498	AC015498	Homo sapi
c1269	40.2	1.7	143205	8	AC093018	AC093018	Oryza sat
1270	40.2	1.7	145427	5	BX276112	BX276112	Zebrafish
1271	40.2	1.7	149662	14	AY077834	AY077834	Sheeppox
1272	40.2	1.7	150057	14	AY077833	AY077833	Sheeppox
1273	40.2	1.7	152009	2	AC010802	AC010802	Homo sapi
c1274	40.2	1.7	156814	8	AP005004	AP005004	Oryza sat
1275	40.2	1.7	162281	9	AC105395	AC105395	Homo sapi
1276	40.2	1.7	171816	9	AC006033	AC006033	Homo sapi
1277	40.2	1.7	171926	2	AC144073	AC144073	Macaca mu
1278	40.2	1.7	173218	2	AP004686	AP004686	Oryza sat
1279	40.2	1.7	173219	2	BX897738	BX897738	Danio rer
c1280	40.2	1.7	189631	2	AC009920	AC009920	Homo sapi
c1281	40.2	1.7	191935	2	AC114747	AC114747	Homo sapi
c1282	40.2	1.7	198944	8	ATCHRIV38	AL161538	Arabidops
c1283	40.2	1.7	199138	2	CR450798	CR450798	Danio rer
c1284	40.2	1.7	200576	8	ATFCA0	Z97335	Arabidopsis
1285	40.2	1.7	203114	2	AC011818	AC011818	Homo sapi
c1286	40.2	1.7	229726	2	AC109699	AC109699	Rattus no
1287	40.2	1.7	235614	2	CR450721	CR450721	Danio rer
c1288	40.2	1.7	280915	2	AC112104	AC112104	Rattus no
1289	40.2	1.7	349980	6	AX344566	AX344566	Sequence
1290	40	1.7	1219	8	AK068336	AK068336	Oryza sat
1291	40	1.7	1350	6	AX653931	AX653931	Sequence
1292	40	1.7	1377	8	BT002638	BT002638	Arabidops
1293	40	1.7	1411	8	BT000356	BT000356	Arabidops
1294	40	1.7	1457	6	AX211618	AX211618	Sequence
1295	40	1.7	1562	8	AY120731	AY120731	Arabidops
1296	40	1.7	1572	8	AY048297	AY048297	Arabidops
1297	40	1.7	1661	8	AK105967	AK105967	Oryza sat
1298	40	1.7	1686	8	AK060997	AK060997	Oryza sat
1299	40	1.7	1696	8	AK103242	AK103242	Oryza sat
1300	40	1.7	1842	8	AK106302	AK106302	Oryza sat
c1301	40	1.7	2026	8	AK117305	AK117305	Arabidops
1302	40	1.7	6029	6	AX346895	AX346895	Sequence
1303	40	1.7	7631	6	AX345762	AX345762	Sequence
1304	40	1.7	8576	6	AX347130	AX347130	Sequence
1305	40	1.7	10716	6	AX346320	AX346320	Sequence
c1306	40	1.7	11985	9	BX322534	BX322534	Human DNA
1307	40	1.7	17389	6	AX346316	AX346316	Sequence
1308	40	1.7	27332	3	CER11A8	Z70310	Caenorhabdi
1309	40	1.7	34548	6	AX349036	AX349036	Sequence
1310	40	1.7	84985	1	SNA278573	AJ278573	Streptomy
1311	40	1.7	94555	9	AL589684	AL589684	Human DNA
1312	40	1.7	97033	2	AC015146	AC015146	Drosophil
c1313	40	1.7	100815	8	ATF12A12	AL133314	Arabidops
1314	40	1.7	104071	2	AL162260	AL162260	Homo sapi

1315	40	1.7	110000	2	AC120698_0	AC120698 Rattus no
1316	40	1.7	110000	2	AC120698_1	Continuation (2 of
c1317	40	1.7	110000	2	BX276116_07	Continuation (8 of
c1318	40	1.7	110000	2	BX276116_08	Continuation (9 of
1319	40	1.7	110000	3	AC116984_1	Continuation (2 of
1320	40	1.7	143508	9	HSJ570L12	AL049589 Human DNA
1321	40	1.7	160366	3	AC069457	AC069457 Drosophil
1322	40	1.7	160776	2	AC137960	AC137960 Mus muscu
1323	40	1.7	168438	2	AC024632	AC024632 Homo sapi
1324	40	1.7	168953	9	AL360219	AL360219 Human DNA
c1325	40	1.7	178433	9	CNS01RHH	AL161752 Human chr
1326	40	1.7	180574	9	AC092807	AC092807 Homo sapi
1327	40	1.7	181927	3	AC010573	AC010573 Drosophil
c1328	40	1.7	182963	2	AC116815	AC116815 Mus muscu
c1329	40	1.7	184470	9	AL589823	AL589823 Human DNA
c1330	40	1.7	220897	2	AL954635	AL954635 Homo sapi
c1331	40	1.7	226142	2	AC126422	AC126422 Mus muscu
c1332	40	1.7	243348	2	AC150646	AC150646 Bos tauru
1333	40	1.7	246640	2	AC108286	AC108286 Rattus no
c1334	40	1.7	265352	2	AC095748	AC095748 Rattus no
1335	40	1.7	278708	3	AE003535	AE003535 Drosophil
c1336	40	1.7	300050	1	AP004171	AP004171 Mycoplasm
1337	40	1.7	349980	6	AX344552	AX344552 Sequence
c1338	39.8	1.7	289	6	AR162089	AR162089 Sequence
c1339	39.8	1.7	289	6	AR166614	AR166614 Sequence
1340	39.8	1.7	993	8	MECGT7	X77464 M.esculenta
1341	39.8	1.7	1371	6	AX412848	AX412848 Sequence
1342	39.8	1.7	1371	6	AX506822	AX506822 Sequence
1343	39.8	1.7	1371	6	AX766276	AX766276 Sequence
1344	39.8	1.7	1371	8	BT000622	BT000622 Arabidops
1345	39.8	1.7	1371	8	BT005368	BT005368 Arabidops
1346	39.8	1.7	1407	6	AX653241	AX653241 Sequence
1347	39.8	1.7	1437	6	AX211638	AX211638 Sequence
c1348	39.8	1.7	1437	6	AX211640	AX211640 Sequence
1349	39.8	1.7	1451	6	AX211616	AX211616 Sequence
1350	39.8	1.7	1494	6	AX211622	AX211622 Sequence
1351	39.8	1.7	1498	8	BT002579	BT002579 Arabidops
1352	39.8	1.7	1516	8	AK118431	AK118431 Arabidops
1353	39.8	1.7	1559	8	AY125506	AY125506 Arabidops
1354	39.8	1.7	1687	8	AY062668	AY062668 Arabidops
c1355	39.8	1.7	1702	3	PFAHGPTA	M88110 Plasmodium
1356	39.8	1.7	2559	6	AX766273	AX766273 Sequence
1357	39.8	1.7	2817	14	AF052502	AF052502 Epiphyas
c1358	39.8	1.7	11086	1	AE010596	AE010596 Fusobacte
1359	39.8	1.7	60193	9	AL359705	AL359705 Human DNA
c1360	39.8	1.7	73184	2	AC090864	AC090864 Homo sapi
c1361	39.8	1.7	79991	2	AC108505	AC108505 Oryza sat
c1362	39.8	1.7	87637	9	AL390960	AL390960 Human DNA
c1363	39.8	1.7	104001	8	AC023628	AC023628 Arabidops
1364	39.8	1.7	107139	2	AL360223	AL360223 Homo sapi
1365	39.8	1.7	108881	8	AC002391	AC002391 Arabidops
1366	39.8	1.7	109659	2	AC151499	AC151499 Dasypus n
c1367	39.8	1.7	110000	2	AC116234_1	Continuation (2 of
1368	39.8	1.7	118584	14	AY043265	AY043265 Epiphyas
1369	39.8	1.7	124186	9	AL772392	AL772392 Human DNA
1370	39.8	1.7	144572	5	BX322794	BX322794 Zebrafish
1371	39.8	1.7	146782	2	AC127599	AC127599 Rattus no

c1372	39.8	1.7	153576	2	AC020572	AC020572	Homo sapi
1373	39.8	1.7	162605	2	AC068698	AC068698	Homo sapi
c1374	39.8	1.7	163088	9	AC097654	AC097654	Homo sapi
1375	39.8	1.7	163364	2	AC116241	AC116241	Rattus no
c1376	39.8	1.7	180005	2	AC136070	AC136070	Rattus no
c1377	39.8	1.7	187651	8	AC129718	AC129718	Oryza sat
c1378	39.8	1.7	189139	2	AC122947	AC122947	Rattus no
c1379	39.8	1.7	198635	2	AC121182	AC121182	Rattus no
1380	39.8	1.7	201427	2	AC127843	AC127843	Rattus no
c1381	39.8	1.7	213678	2	AC137173	AC137173	Rattus no
c1382	39.8	1.7	215675	2	AC123264	AC123264	Rattus no
c1383	39.8	1.7	220283	2	AC103391	AC103391	Mus muscu
c1384	39.8	1.7	221631	9	AC010867	AC010867	Homo sapi
c1385	39.8	1.7	224818	2	AC111839	AC111839	Rattus no
c1386	39.8	1.7	231770	2	AC109171	AC109171	Mus muscu
1387	39.8	1.7	238637	2	AC092254	AC092254	Mus muscu
1388	39.8	1.7	245515	2	AC151275	AC151275	Mus muscu
1389	39.8	1.7	245795	2	AC096419	AC096419	Rattus no
1390	39.8	1.7	249487	2	AC095161	AC095161	Rattus no
1391	39.8	1.7	250178	2	AC118121	AC118121	Rattus no
c1392	39.8	1.7	253188	2	AC098354	AC098354	Rattus no
1393	39.8	1.7	273729	2	AC106147	AC106147	Rattus no
c1394	39.8	1.7	277363	2	AC134745	AC134745	Rattus no
1395	39.8	1.7	286451	2	AC115130	AC115130	Rattus no
c1396	39.8	1.7	299467	2	AC120784	AC120784	Mus muscu
1397	39.6	1.7	1231	1	AY234840	AY234840	Staphyloc
1398	39.6	1.7	1368	14	AF166115	AF166115	Potato vi
1399	39.6	1.7	1387	8	AY117336	AY117336	Arabidops
1400	39.6	1.7	1419	6	AX653260	AX653260	Sequence
1401	39.6	1.7	1433	6	AX211617	AX211617	Sequence
1402	39.6	1.7	1443	14	PVYDNA0	Z50042	Potato viru
1403	39.6	1.7	1443	14	PVYDNA1	Z50041	Potato viru
1404	39.6	1.7	1443	14	PVYDNAONA	Z50043	Potato viru
1405	39.6	1.7	1596	8	AY084880	AY084880	Arabidops
1406	39.6	1.7	1689	8	AY080716	AY080716	Arabidops
1407	39.6	1.7	1980	14	BSU61154	U61154	Buzura supp
c1408	39.6	1.7	5858	3	AF350276	AF350276	Nephila m
1409	39.6	1.7	6104	6	AX346269	AX346269	Sequence
c1410	39.6	1.7	8004	6	CQ588884	CQ588884	Sequence
1411	39.6	1.7	8033	3	PPINMP	Y13117	Paramecium
c1412	39.6	1.7	8736	6	CQ588875	CQ588875	Sequence
1413	39.6	1.7	9958	3	AF246689	AF246689	Dictyoste
1414	39.6	1.7	12500	3	AF482381	AF482381	Dictyoste
1415	39.6	1.7	15052	1	AF055579	AF055579	Streptomy
c1416	39.6	1.7	34919	3	AF100663	AF100663	Caenorhab
c1417	39.6	1.7	37225	9	AC005954	AC005954	Homo sapi
1418	39.6	1.7	49817	2	AC013939	AC013939	Drosophil
1419	39.6	1.7	50937	6	AR159871	AR159871	Sequence
c1420	39.6	1.7	53920	9	AC116423	AC116423	Homo sapi
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1422	39.6	1.7	74492	8	AY350713	AY350713	Capsella
c1423	39.6	1.7	83528	8	AP005695	AP005695	Oryza sat
c1424	39.6	1.7	85916	3	AC117080	AC117080	Dictyoste
c1425	39.6	1.7	103908	2	AC150245	AC150245	Medicago
c1426	39.6	1.7	128018	2	BX890615	BX890615	Danio rer
c1427	39.6	1.7	138158	5	BX005232	BX005232	Zebrafish
1428	39.6	1.7	139147	2	AC006725	AC006725	Caenorhab

c1429	39.6	1.7	148397	2	CR751563	CR751563	Danio rer
1430	39.6	1.7	150876	2	AC108761	AC108761	Oryza sat
1431	39.6	1.7	154082	2	AC108756	AC108756	Oryza sat
c1432	39.6	1.7	154195	2	AC013641	AC013641	Homo sapi
c1433	39.6	1.7	167195	3	AC007808	AC007808	Drosophil
1434	39.6	1.7	170425	5	BX465867	BX465867	Zebrafish
1435	39.6	1.7	179399	5	AL929338	AL929338	Zebrafish
c1436	39.6	1.7	185672	2	BX640474	BX640474	Danio rer
1437	39.6	1.7	187495	9	AC026887	AC026887	Homo sapi
1438	39.6	1.7	188638	2	CR759889	CR759889	Danio rer
1439	39.6	1.7	210700	2	AC103382	AC103382	Mus muscu
1440	39.6	1.7	212134	2	AC024037	AC024037	Homo sapi
1441	39.6	1.7	212499	2	CR626887	CR626887	Danio rer
c1442	39.6	1.7	215210	2	CR749744	CR749744	Danio rer
1443	39.6	1.7	219892	2	AC127200	AC127200	Rattus no
1444	39.6	1.7	220817	2	AC113854	AC113854	Rattus no
1445	39.6	1.7	226092	2	AC107090	AC107090	Rattus no
c1446	39.6	1.7	233220	2	AC098058	AC098058	Rattus no
1447	39.6	1.7	254633	2	CR762389	CR762389	Danio rer
1448	39.6	1.7	254733	3	AC117075	AC117075	Dictyoste
c1449	39.6	1.7	254961	3	AE003706	AE003706	Drosophil
1450	39.6	1.7	269863	2	AC131017	AC131017	Rattus no
1451	39.4	1.7	640	6	AX652149	AX652149	Sequence
1452	39.4	1.7	1437	6	AX211602	AX211602	Sequence
1453	39.4	1.7	1437	6	AX651766	AX651766	Sequence
1454	39.4	1.7	1479	8	AB191246	AB191246	Dianthus
1455	39.4	1.7	1918	8	AK102481	AK102481	Oryza sat
c1456	39.4	1.7	1921	6	CQ577878	CQ577878	Sequence
c1457	39.4	1.7	2055	8	AK106646	AK106646	Oryza sat
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1461	39.4	1.7	11155	6	AX345507	AX345507	Sequence
c1462	39.4	1.7	38801	3	CEK09B11	Z83114	Caenorhabdi
c1463	39.4	1.7	39329	9	AC004091	AC004091	Human Cos
c1464	39.4	1.7	43644	9	AC004092	AC004092	Human Cos
1465	39.4	1.7	47108	6	AX344507	AX344507	Sequence
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c1469	39.4	1.7	99699	2	AC013845	AC013845	Drosophil
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c1471	39.4	1.7	127131	8	AC146819	AC146819	Medicago
c1472	39.4	1.7	128223	8	AP005643	AP005643	Oryza sat
c1473	39.4	1.7	131734	2	CR792420	CR792420	Danio rer
1474	39.4	1.7	136471	8	AP003622	AP003622	Oryza sat
1475	39.4	1.7	138850	8	AC133341	AC133341	Medicago
1476	39.4	1.7	140757	9	AL157778	AL157778	Human DNA
c1477	39.4	1.7	144022	5	BX088594	BX088594	Zebrafish
c1478	39.4	1.7	147245	8	AP003217	AP003217	Oryza sat
1479	39.4	1.7	147640	2	AP003542	AP003542	Oryza sat
1480	39.4	1.7	155906	8	AP005934	AP005934	Oryza sat
c1481	39.4	1.7	160285	2	CR848001	CR848001	Danio rer
1482	39.4	1.7	168269	2	CR352217	CR352217	Danio rer
1483	39.4	1.7	171165	2	CR376767	CR376767	Danio rer
1484	39.4	1.7	172854	3	AC023706	AC023706	Drosophil
c1485	39.4	1.7	175947	8	AP003435	AP003435	Oryza sat

1486	39.4	1.7	177743	9	AC105941	AC105941 Homo sapi
c1487	39.4	1.7	183648	3	AC117081	AC117081 Dictyoste
c1488	39.4	1.7	186739	9	AC072028	AC072028 Homo sapi
1489	39.4	1.7	189441	2	AC022989	AC022989 Homo sapi
c1490	39.4	1.7	190930	2	BX936353	BX936353 Danio rer
1491	39.4	1.7	191590	3	AC023722	AC023722 Drosophil
c1492	39.4	1.7	192634	2	AC069466	AC069466 Mus muscu
1493	39.4	1.7	197419	8	ATCHRIV41	AL161541 Arabidops
1494	39.4	1.7	198019	5	BX469910	BX469910 Zebrafish
1495	39.4	1.7	198946	10	AL844548	AL844548 Mouse DNA
1496	39.4	1.7	200252	8	ATFCA3	Z97338 Arabidopsis
c1497	39.4	1.7	205225	2	CR812896	CR812896 Danio rer
1498	39.4	1.7	216131	5	BX005004	BX005004 Zebrafish
c1499	39.4	1.7	224731	2	AC105545	AC105545 Rattus no
1500	39.4	1.7	273275	3	AE014828	AE014828 Plasmodiu

ALIGNMENTS

RESULT 1

AX697213

LOCUS AX697213 2320 bp DNA linear PAT 02-APR-2003

DEFINITION Sequence 281 from Patent WO0078961.

ACCESSION AX697213

VERSION AX697213.1 GI:29498151

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: WO 0078961-A 281 28-DEC-2000;
Genentech Inc. (US)

FEATURES Location/Qualifiers
source 1. .2320
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2320; DB 6; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60
|||||

Db 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
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Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
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Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
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Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
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Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
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Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
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Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960

Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAAGTGTTCATTGGCCCAA	1080
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
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Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
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Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCCTATGTCTTTCAGCA	1500
Db	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCCTATGTCTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
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Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
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Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
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Qy	1681	TCACCATTCTAGGGAGCTTCCCAGTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
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 Db 1801 ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT 1860

Qy 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920
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 Db 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920

Qy 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
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Qy 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
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Qy 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
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 Db 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100

Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
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 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160

Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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 Db 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320

RESULT 2

AY358416

LOCUS AY358416 2320 bp mRNA linear PRI 03-OCT-2003

DEFINITION Homo sapiens clone DNA71169 glucuronosyltransferase (UNQ842) mRNA, complete cds.

ACCESSION AY358416

VERSION AY358416.1 GI:37181956

KEYWORDS FLI_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2320)

AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,

Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
 Goddard,A., Wood,W.I. and Godowski,P.

TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment

JOURNAL Genome Res. 13 (10), 2265-2270 (2003)

PUBMED 12975309

REFERENCE 2 (bases 1 to 2320)

AUTHORS Clark,H.F.

TITLE Direct Submission

JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES Location/Qualifiers

source 1. .2320
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gene 1. .2320
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CDS 68. .1639
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ORIGIN

Query Match 100.0%; Score 2320; DB 9; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
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Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCCTTCTTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Db	61	AGTGAGCATGGCTGGGCAGCGAGTGCCTTCTTAGTGGGCTTCCTTCTCCCTGGGGTCCT	120
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240

Db	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Db	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Db	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA	360
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Db	541	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACC	600
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080

Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1381	GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Qy	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA	1500
Db	1441	GATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA	1500
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Qy	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1681	TCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Db	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Db	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT	1860
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920

Qy 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980
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 Db 1921 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 1980

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 Db 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040

Qy 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
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 Db 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100

Qy 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160
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 Db 2101 TTCTGTTTTGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG 2160

Qy 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220
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 Db 2161 AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA 2220

Qy 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280
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 Db 2221 CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA 2280

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RESULT 3

AX136141

LOCUS AX136141 2341 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 63 from Patent EP1067182.

ACCESSION AX136141

VERSION AX136141.1 GI:14272549

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
 Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: EP 1067182-A 63 10-JAN-2001;

Helix Research Institute (JP)

FEATURES Location/Qualifiers

source 1. .2341

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CDS 94. .1665

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ORIGIN

Query Match 99.6%; Score 2310.2; DB 6; Length 2341;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
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Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	147	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	206
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	207	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	266
Qy	241	CAAAGAGGTCCTTTTATGCCAGATTTTAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Db	267	CAAAGAGGTCCTTTTATGCCAGATTTTAAAAGGAAGAAAATCATATCAAGTTATCAG	326
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAGAGTTTGAATTCCTTCTGGA	360
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Qy	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	387	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	446
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA	480
Db	447	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAA	506
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	507	CTTCGACATGGTGATAGTTGAAACTTTTACTACTGTCCTTTCCTGATTGCTGAGAAGCT	566
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Db	567	TGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTCCGGCTCTTGGAAATTTGGGCTACC	626
Qy	601	AATCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660

Db	627	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	686
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	687	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	746
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTG	780
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Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
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Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	867	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	926
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	927	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	986
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	987	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1046
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTTGGCCCAA	1080
Db	1047	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTTGGCCCAA	1106
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1107	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1166
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1167	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1226
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1227	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1286
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1287	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTTCAGTTAAAGAAGCTCAAGGCAGA	1346
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1347	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1406
Qy	1381	GGCTGCCAGTGTGATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1407	GGCTGCCAGTGTGATCCTGCGCTCCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1466
Qy	1441	GATTGACCACGTCTTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTTCAGCA	1500
Db	1467	GATTGACCACGTCTTCCAGACAGGGGGCGGACGCACCTCAAGCCCTATGTCTTTTCAGCA	1526

Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1527	GCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1586
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1587	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1646
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1647	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1706
Qy	1681	TCACCATTTCTAGGGAGCTTCCCAGTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1707	TCACCATTTCTAGGGAGCTTCCCAGTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1766
Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1800
Db	1767	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGCTA	1826
Qy	1801	ATTTTGGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1860
Db	1827	ATTTTGGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT	1886
Qy	1861	CTTGTCTCCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1887	CTTGTCTCCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1946
Qy	1921	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	1980
Db	1947	TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC	2006
Qy	1981	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2040
Db	2007	CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC	2066
Qy	2041	TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT	2100
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Qy	2101	TTCTGTTTTGTCTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2160
Db	2127	TTCTGTTTTGTCTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAG	2186
Qy	2161	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2220
Db	2187	AGTTCAGGGCCGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCCA	2246
Qy	2221	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2280
Db	2247	CAGTGAGCTCCTTCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAA	2306
Qy	2281	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC	2315
Db	2307	AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTC	2341

RESULT 4

BD123523

LOCUS BD123523 2341 bp DNA linear PAT 18-SEP-2002

DEFINITION Secretory protein or membrane protein.

ACCESSION BD123523

VERSION BD123523.1 GI:23218468

KEYWORDS JP 2002017376-A/32.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2341)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: JP 2002017376-A 32 22-JAN-2002;

HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)

PN JP 2002017376-A/32

PD 22-JAN-2002

PF 07-JUL-2000 JP 2000253173

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU

PI SUGIYAMA,

PI KOJI HAYASHI

PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10, PC

PC C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC

Secretory protein or membrane protein

FH Key Location/Qualifiers

FT CDS (94)..(1662).

FEATURES Location/Qualifiers

source

1..2341

/organism="Homo sapiens"

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ORIGIN

Query Match 99.6%; Score 2310.2; DB 6; Length 2341;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

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Db 27 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 86

Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120

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Db 87 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 146

Qy 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180

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Db 147 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 206

Qy 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240

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Db	207	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	266
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Db	267	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAG	326
Qy	301	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	360
Db	327	TTGGCTTGCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGA	386
Qy	361	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	387	AGAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	446
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	447	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	506
Qy	481	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	507	CTTCGACATGGTGATAGTTGAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	566
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	600
Db	567	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC	626
Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	660
Db	627	AATCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTG	686
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	687	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	746
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTC	780
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Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	807	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	866
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	867	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	926
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	960
Db	927	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCCTTGT	986
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	987	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1046
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1080
Db	1047	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCCCAA	1106

Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1107	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1166
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1167	GGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAGAATAGCATAATGGAGGC	1226
Qy	1201	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1260
Db	1227	CATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACAT	1286
Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1287	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1346
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
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Qy	1381	GGCTGCCAGTGTATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1407	GGCTGCCAGTGTATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1466
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA	1500
Db	1467	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTTCAGCA	1526
Qy	1501	GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1527	GCCCTGGCATGAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1586
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1587	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1646
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
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Db	1887	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGA	1946

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 Db 1947 TGGACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCCTCTC 2006
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 Qy 1981 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2040
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 Db 2007 CGAATCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCC 2066
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 Qy 2041 TGCCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGT 2100
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RESULT 5

AK075383

LOCUS AK075383 2341 bp mRNA linear PRI 03-SEP-2002
 DEFINITION Homo sapiens cDNA PSEC0073 fis, clone NT2RP2002934, weakly similar to UDP-GLUCURONOSYLTRANSFERASE 2C1 MICROSOMAL (EC 2.4.1.17).

ACCESSION AK075383

VERSION AK075383.1 GI:22761433

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
 AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K., Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.

TITLE HRI human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2341)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT

HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing; Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction: Institute of Medical Science, University

of Tokyo, Laboratory of Genome Structure, Human Genome Center.

FEATURES

source

Location/Qualifiers

1. .2341

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/mol_type="mRNA"

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/cell_line="NT2"

/cell_type="teratocarcinoma"

/clone_lib="NT2RP2"

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CDS

94. .1665

/note="unnamed protein product"

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STFDNTIKEHFTGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMKPI
KPVPQDLENFIAKFEDSGFVLVTLGSMVNTCQNPFIKEMNNAFAHLPGQVIWKQCS
HWPQDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVGIPLFG
DQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAVAASVILRSHPLS
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ORIGIN

Query Match 99.6%; Score 2310.2; DB 9; Length 2341;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2312; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTCT	120
Db	87	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTCT	146
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	147	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	206
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
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Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGC	420
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Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	507	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	566
Qy	541	TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACC	600
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Qy	601	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	660
Db	627	AATCCCCTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTG	686
Qy	661	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	720
Db	687	GGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCA	746
Qy	721	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	780
Db	747	GTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTGTC	806
Qy	781	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	840
Db	807	TCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGC	866
Qy	841	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	900
Db	867	TCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAAACC	926
Qy	901	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	960
Db	927	AGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTTGT	986
Qy	961	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1020
Db	987	GACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAACAA	1046
Qy	1021	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA	1080
Db	1047	TGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTCAGTGTTCTCATTGGCCCAA	1106
Qy	1081	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1140
Db	1107	AGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCCTCAGAGTGACCTCCT	1166
Qy	1141	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1200
Db	1167	GGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCGGGCAGAATAGCATAATGGAGGC	1226

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Qy	1261	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1320
Db	1287	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1346
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Qy	1381	GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1407	GGCTGCCAGTGTTCATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1466
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
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Qy	1501	GCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1560
Db	1527	GCCCTGGCATGAGCAGTACCTGCTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGG	1586
Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
Db	1587	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1646
Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
Db	1647	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1706
Qy	1681	TCACCATTTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
Db	1707	TCACCATTTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1766
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Db	1767	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACCTTGCTA	1826
Qy	1801	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1860
Db	1827	ATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCAGTCCT	1886
Qy	1861	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1920
Db	1887	CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT	1946
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RESULT 6

AX548037

LOCUS AX548037 2944 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 13 from Patent WO02066654.

ACCESSION AX548037

VERSION AX548037.1 GI:25813133

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Astromoff,A., Au-Young,J., Baughn,M.R., Ding,L., Duggan,B.M.,
Forsythe,I.J., Gietzen,K.J., Griffin,J.A., Lee,E.A., Lu,Y.,
Richardson,T.W., Ring,H.Z., Sanjanwala,M.M., Swarnakar,A.,
Walia,N.K., Warren,B.A., Xu,Y., Yue,H. and Zebarjadian,Y.

TITLE Drug metabolizing enzymes

JOURNAL Patent: WO 02066654-A 13 29-AUG-2002;

Incyte Genomics, Inc. (US)

FEATURES

Location/Qualifiers

source

1. .2944

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/mol_type="unassigned DNA"

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Query Match 90.6%; Score 2102.8; DB 6; Length 2944;

Best Local Similarity 95.5%; Pred. No. 0;

Matches 2216; Conservative 0; Mismatches 2; Indels 102; Gaps 1;

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Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
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Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	462	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	521
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Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540
Db	582	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	641
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Db	1362	GGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTTCAGTTAAAGAAGCTCAAGGCAGA	1421
Qy	1321	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1380
Db	1422	GACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGATACAAGTCCGCGGCAGT	1481
Qy	1381	GGCTGCCAGTGTATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1440
Db	1482	GGCTGCCAGTGTATCCTGCGCTCCACCCGCTCAGCCCCACACAGCGGCTGGTGGGCTG	1541
Qy	1441	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1500
Db	1542	GATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTATGTCTTTCAGCA	1601
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Qy	1561	GACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAG	1620
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Qy	1621	AAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGGGCGATG	1680
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Qy	1681	TCACCATTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTTCTAGT	1740
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Qy	1741	TATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGCTA	1800
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 Qy 1861 CTTGTCCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACT 1920
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 Qy 2281 AATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCACTAA 2320
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RESULT 7

AX958403

LOCUS AX958403 2263 bp DNA linear PAT 14-JAN-2004

DEFINITION Sequence 31 from Patent WO0226988.

ACCESSION AX958403

VERSION AX958403.1 GI:40879361

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS .

TITLE Human drug metabolizing enzymes

JOURNAL Patent: WO 0226988-A 31 04-APR-2002;

Incyte Genomics, Inc. (US)

FEATURES

source

Location/Qualifiers

1. .2263

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ORIGIN

Query Match 68.1%; Score 1578.8; DB 6; Length 2263;
Best Local Similarity 92.6%; Pred. No. 0;
Matches 1658; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

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Db 1282 AGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTTAAAGAAGCTCAAGGCAGAGACATT 1341

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RESULT 8

AX359921

LOCUS AX359921 2082 bp DNA linear PAT 13-FEB-2002

DEFINITION Sequence 1 from Patent WO0202774.

ACCESSION AX359921

VERSION AX359921.1 GI:18675563

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Leiby, K.R., Cook, W.J. and Spaltmann, F.

TITLE 32626, a human udp-glycosyltransferase and uses thereof

JOURNAL Patent: WO 0202774-A 1 10-JAN-2002;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES

source Location/Qualifiers

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CDS

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ORIGIN

Query Match 55.2%; Score 1281.6; DB 6; Length 2082;

Best Local Similarity 85.9%; Pred. No. 0;

Matches 1422; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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Qy	127	AGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA	186
Db	204	AGAGGCTGCCAAAATCCTGACAATATCTACACTGGGTGGAAGCCATTACCTACTGTTGGA	263
Qy	187	CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAG	246
Db	264	CCGGGTGTCTCAGATTCTTCAAGAGCATGGTCATAATGTGACTATGCTTCATCAGAGTGG	323
Qy	247	AGGTCCTTTTTATGCCAGATTTTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCT	306
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Qy	367	TTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCA	426
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Db	564	TCTGGTATTTGTTGAAGCATTTGATTTCTGTTCTTTCTGATTGCTGAGAAGCTTGTGAA	623
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Qy	607	CTTGCTTATGTTCCAGTATTCCGTTCTTTGCTGACTGATCACATGGACTTCTGGGGCCG	666
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Qy	667	AGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTAC	726
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Qy	727	ATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCT	786
Db	804	ATTTGACAACACCATCAAGGAGCATTTCCAGAAGGCTCTAGGCCAGTTTTGTCTCATCT	863
Qy	787	TCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACC	846
Db	864	TCTACTGAAAGCAGAGTTGTGGTTTGTAACTCTGATTTTGCCTTTGATTTTGCCCGGCC	923
Qy	847	TCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAACCTATTAAACCAGTACC	906

LOCUS AX155211 2797 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 1 from Patent WO0138505.
 ACCESSION AX155211
 VERSION AX155211.1 GI:14536690
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Adler,D.A., Dong,D.L., Pownder,S., Gao,Z. and Conklin,D.C.
 TITLE Secretd protein, zalpha37
 JOURNAL Patent: WO 0138505-A 1 31-MAY-2001;
 ZymoGenetics, Inc. (US)

FEATURES Location/Qualifiers
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ORIGIN

Query Match 55.2%; Score 1281.6; DB 6; Length 2797;
 Best Local Similarity 85.9%; Pred. No. 0;
 Matches 1422; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

Qy 7 CCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAAGTGAG 66
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 Db 58 CCTTAGCCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCTGCTTCTGTGGAAGTGAG 117
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Db	358	TTCACCTGAAGATCATCAAAAAGAATTAAGAAGCATTGATAGCTACATAGAAACAGC	417
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Helix Research Institute (JP) ; Research Association for
Biotechnology (JP)

FEATURES Location/Qualifiers
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ORIGIN

Query Match 55.2%; Score 1281.6; DB 6; Length 2823;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1422; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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Qy     67  CATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTTGCTCTC 126
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Qy    127  AGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA 186
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JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
 PUBMED 14702039
 REFERENCE 2
 AUTHORS Kawakami,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Irie,R.,
 Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
 Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
 Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
 Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
 Oshima,A., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K.
 and Isogai,T.
 TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 2823)
 AUTHORS Isogai,T., Otsuki,T. and Sugiyama,T.
 TITLE Direct Submission
 JOURNAL Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: RAB and
 HRI.

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ORIGIN

Query Match 55.2%; Score 1281.6; DB 9; Length 2823;
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 Matches 1422; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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Db 937 CCTGCTTCCCAACACTGTTTATATTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACC 996

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 VERSION BC068446.1 GI:46250395
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2759)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 2759)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (02-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24432082.

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Db	421	TGTAGTTATTTGCTAAGCAGAAAGGATATAATGGATTCCCTTAAAGAATGAGAACTATGAT	480
Qy	488	ATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAG	547
Db	481	CTGGTATTTGTTGAAGCATTTGATTTCTGTTCTTTCCTGATTGCTGAGAAGCTTGTGAAA	540
Qy	548	CCATTTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACCAATCCCC	607
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Qy	608	TTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCGA	667
Db	601	TTGTCTTATGTTCCAGTATTCCCTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGA	660
Qy	668	GTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACA	727
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Qy	728	TTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTT	787
Db	721	TTTGACAACACCATCAAGGAGCATTTCCAGAAGGCTCTAGGCCAGTTTGTCTCATCTT	780
Qy	788	CTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACCT	847
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Db	901	CAAGACTTGAGAACTTCATTGCCAAGTTTGGGGATGCAGGTTTGTCTTGTGGCCTTT	960
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Db	1021	GCCACCTCCCTCAAGGAGTGATATGGACATGTCAGAGTCTCATTGGCCCAAGAGATGTT	1080
Qy	1088	CACCTGGCTGCAAATGTGAAAATGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCAC	1147
Db	1081	CATTTGGCCACAAATGTGAAAATGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCAC	1140

Qy	1148	CCAAGCATCCCGTCTGTTTGTCACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAG	1207
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Qy	1208	CATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGA	1267
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Qy	1508	CATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTA	1567
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Qy	1568	TGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTG	1627
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RESULT 13

AX327327

LOCUS	AX327327	2086 bp	DNA	linear	PAT 07-JAN-2002
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DEFINITION Sequence 12 from Patent WO0179468.

ACCESSION AX327327

VERSION AX327327.1 GI:18097873

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Policky, J. L., Hafalia, A., Burford, N., Ring, H. Z., Lal, P.,
Tribouley, C. M., Yao, M. G., Yue, H., Tang, Y. T., Patterson, C., Das, D.,
Sanjanwala, M. S., Gandhi, A. R., Reddy, R., Khan, F. A., Baughn, M. R.,
Ramkumar, J., Griffin, J. A. and Au-Young, J.

TITLE Drug metabolizing enzymes

JOURNAL Patent: WO 0179468-A 12 25-OCT-2001;

FEATURES	Incyte Genomics, Inc. (US) Location/Qualifiers
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source 1. .2086
/organism="Homo sapiens"
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ORIGIN

Query Match 55.2%; Score 1280; DB 6; Length 2086;
Best Local Similarity 85.8%; Pred. No. 0;
Matches 1421; Conservative 0; Mismatches 235; Indels 0; Gaps 0;

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RESULT 14

AX359923

LOCUS AX359923 1572 bp DNA linear PAT 13-FEB-2002

DEFINITION Sequence 3 from Patent WO0202774.

ACCESSION AX359923

VERSION AX359923.1 GI:18675565

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Leiby, K.R., Cook, W.J. and Spaltmann, F.

TITLE 32626, a human udp-glycosyltransferase and uses thereof

JOURNAL Patent: WO 0202774-A 3 10-JAN-2002;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES

source

Location/Qualifiers

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/db_xref="taxon:9606"

ORIGIN

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Best Local Similarity 85.7%; Pred. No. 1.8e-310;

Matches 1347; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

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Qy	608	TTGTCTTATGTTCCAGTATTCCGTTCCCTGCTGACTGATCACATGGACTTCTGGGGCCGA	667
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AR541778

LOCUS	AR541778	2426 bp	DNA	linear	PAT 08-OCT-2004
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DEFINITION Sequence 26 from patent US 6743619.

ACCESSION AR541778
VERSION AR541778.1 GI:53933858

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2426)

TITLE Nucleic acids and polypeptides

JOURNAL Patent: US 6743619-A 26 01-JUN-2004;

FEATURES	Location/Qualifiers
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Query Match 49.5%; Score 1147.8; DB 6; Length 2426;

Best Local Similarity 85.2%; Pred. No. 2.2e-293;

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GenCore version 5.1.6

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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAC58107	standard;	cdna;	2320	BP.	
DE	Human	PRO1780	nucleotide	sequence	SEQ ID NO:12.	
PN	WO200053750-A1.					
PD	14-SEP-2000.					
PA	(GETH)	GENENTECH	INC.			
	Query Match	100.0%;	Score 2320;	DB 3;	Length 2320;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 2						
ID	AAA37101	standard;	cdna;	2320	BP.	
DE	Human	PRO1780 (UNQ842)	cdna	sequence	SEQ ID NO:281.	
PN	WO200012708-A2.					
PD	09-MAR-2000.					
PA	(GETH)	GENENTECH	INC.			
	Query Match	100.0%;	Score 2320;	DB 3;	Length 2320;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 3						
ID	AAF54401	standard;	dna;	2320	BP.	
DE	Primer #82	used in the	identification	of	proteins.	
PN	WO200078961-A1.					
PD	28-DEC-2000.					
PA	(GETH)	GENENTECH	INC.			

Query Match 100.0%; Score 2320; DB 4; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 4

ID ACD68440 standard; cDNA; 2320 BP.
 DE Novel human secreted and transmembrane protein PRO1780 cDNA.
 PN US2003073130-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 9; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 5

ID ACH04542 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003044841-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 9; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 6

ID ACD68086 standard; cDNA; 2320 BP.
 DE Novel human secreted and transmembrane protein PRO1780 cDNA.
 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 9; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 7

ID ADC18150 standard; cDNA; 2320 BP.
 DE Human PRO polynucleotide #80.
 PN US2003064925-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 8

ID ADD70796 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003099625-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 9

ID ADD39873 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003083462-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 10

ID ADD70319 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003054406-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 11

ID ADD38440 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003096955-A1.

PD 22-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 12

ID ADD39396 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003096954-A1.

PD 22-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 13

ID ADD38919 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003092061-A1.

PD 15-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 14

ID ADD40350 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003082627-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 15

ID ADE50571 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003069179-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 16

ID ADE20183 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003092883-A1.

PD 15-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 17

ID ADE50094 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.

PN US2003082626-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2320; DB 10; Length 2320;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 18

ID ADE21652 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 19

ID ADF30077 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 20

ID ADF55970 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 21

ID ADH99474 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 10; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 22

ID ADE96654 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 23

ID ADF25965 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 24

ID ADF24864 standard; cDNA; 2320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1780.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2320; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 25

ID ADF29600 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003203401-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 26
 ID ADE97131 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003195334-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 27
 ID ADH03169 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003216562-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 28
 ID ADH04123 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003220471-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 29
 ID ADH03646 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2003224478-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 30
 ID ADH04600 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2004005626-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 31
 ID ADH61601 standard; cDNA; 2320 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2004014130-A1.
 PD 22-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 32
 ID ADL94800 standard; cDNA; 2320 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1780.
 PN US2004073015-A1.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2320; DB 12; Length 2320;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 33
 ID AAF93775 standard; cDNA; 2341 BP.
 DE Human cDNA encoding a membrane or secretory protein clone PSEC0073.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 99.6%; Score 2310.2; DB 5; Length 2341;
 Best Local Similarity 99.9%; Pred. No. 0;
 RESULT 34
 ID AAL41485 standard; DNA; 2944 BP.
 DE Drug metabolising enzyme encoding DNA - 7486594CB1.
 PN WO200266654-A2.
 PD 29-AUG-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 90.6%; Score 2102.8; DB 6; Length 2944;
 Best Local Similarity 95.5%; Pred. No. 0;
 RESULT 35
 ID AAS62475 standard; cDNA; 2074 BP.
 DE cDNA sequence #262 encoding novel human secreted protein.
 PN WO200177291-A2.
 PD 18-OCT-2001.
 PA (GEMY) GENETICS INST INC.
 Query Match 88.9%; Score 2063.4; DB 6; Length 2074;
 Best Local Similarity 99.7%; Pred. No. 0;
 RESULT 36
 ID ADR19692 standard; DNA; 2263 BP.
 DE Human drug metabolising enzyme (DME)-13 gene sequence.
 PN WO200226988-A2.
 PD 04-APR-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 68.1%; Score 1578.8; DB 7; Length 2263;
 Best Local Similarity 92.6%; Pred. No. 0;
 RESULT 37
 ID AAD06821 standard; cDNA; 2797 BP.
 DE Human secreted protein Zalpa37 cDNA.
 PN WO200138505-A2.
 PD 31-MAY-2001.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 55.2%; Score 1281.6; DB 4; Length 2797;
 Best Local Similarity 85.9%; Pred. No. 0;
 RESULT 38
 ID ADA53720 standard; cDNA; 2823 BP.
 DE Human coding sequence, SEQ ID 1288.
 PN EP1293569-A2.
 PD 19-MAR-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 55.2%; Score 1281.6; DB 10; Length 2823;
 Best Local Similarity 85.9%; Pred. No. 0;
 RESULT 39
 ID AAD24667 standard; cDNA; 2086 BP.

DE Human drug metabolising enzyme (DME)-2 cDNA.
 PN WO200179468-A2.
 PD 25-OCT-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 55.2%; Score 1280; DB 6; Length 2086;
 Best Local Similarity 85.8%; Pred. No. 0;

RESULT 40
 ID ABK90831 standard; cDNA; 1851 BP.
 DE cDNA encoding drug metabolising enzyme.
 PN US2002082194-A1.
 PD 27-JUN-2002.
 PA (GUEG/) GUEGLER K.
 PA (WEBS/) WEBSTER M.
 PA (YANC/) YAN C.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 Query Match 54.8%; Score 1270.4; DB 6; Length 1851;
 Best Local Similarity 85.9%; Pred. No. 0;

RESULT 41
 ID ADN02571 standard; DNA; 2868 BP.
 DE Human hepatouracil dinucleotide glycosyltransferase 29.7 DNA.
 PN CN1393551-A.
 PD 29-JAN-2003.
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 Query Match 54.5%; Score 1264.8; DB 11; Length 2868;
 Best Local Similarity 85.6%; Pred. No. 0;

RESULT 42
 ID AAD25345 standard; cDNA; 2082 BP.
 DE Human UDP-glycosyltransferase, 32626 cDNA.
 PN WO200202774-A2.
 PD 10-JAN-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 54.2%; Score 1257.6; DB 6; Length 2082;
 Best Local Similarity 85.0%; Pred. No. 0;

RESULT 43
 ID ABL57726 standard; DNA; 1572 BP.
 DE Human sbg10054OUDPGT gene #2.
 PN WO200222802-A1.
 PD 21-MAR-2002.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 Query Match 52.2%; Score 1212; DB 6; Length 1572;
 Best Local Similarity 85.7%; Pred. No. 0;

RESULT 44
 ID ADA21188 standard; cDNA; 2268 BP.
 DE Human secreted protein SECP-42 encoding cDNA SEQ ID NO:93.
 PN WO2003068943-A2.
 PD 21-AUG-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 49.5%; Score 1147.8; DB 9; Length 2268;
 Best Local Similarity 85.2%; Pred. No. 0;

RESULT 45
 ID ABX70800 standard; cDNA; 2426 BP.
 DE Novel human cDNA sequence #25.
 PN WO200281731-A2.
 PD 17-OCT-2002.

PA (HYSE-) HYSEQ INC.
PA (GOOD/) GOODRICH R W.
Query Match 49.5%; Score 1147.8; DB 8; Length 2426;
Best Local Similarity 85.2%; Pred. No. 0;
RESULT 46
ID ADQ75567 standard; cDNA; 2791 BP.
DE Uridine diphosphate-galactosyl ceramide glucuronyl collagen transferase.
PN CN1380409-A.
PD 20-NOV-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 49.5%; Score 1147.8; DB 11; Length 2791;
Best Local Similarity 85.2%; Pred. No. 0;
RESULT 47
ID ABL57725 standard; DNA; 1182 BP.
DE Human sbg10054OUDPGT gene #1.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 41.2%; Score 956.4; DB 6; Length 1182;
Best Local Similarity 88.1%; Pred. No. 4.4e-274;
RESULT 48
ID AAD06822 standard; DNA; 1569 BP.
DE Human secreted protein Zalpa37 degenerate coding sequence.
PN WO200138505-A2.
PD 31-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 40.7%; Score 944.8; DB 4; Length 1569;
Best Local Similarity 52.4%; Pred. No. 1.5e-270;
RESULT 49
ID AAD06823 standard; cDNA; 2212 BP.
DE Mouse secreted protein Zalpa37 cDNA.
PN WO200138505-A2.
PD 31-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 39.3%; Score 910.8; DB 4; Length 2212;
Best Local Similarity 73.0%; Pred. No. 2.8e-260;
RESULT 50
ID AAS84832 standard; cDNA; 2721 BP.
DE DNA encoding novel human diagnostic protein #20636.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 34.9%; Score 808.8; DB 5; Length 2721;
Best Local Similarity 95.8%; Pred. No. 9.2e-230;
RESULT 51
ID AAD06824 standard; DNA; 1569 BP.
DE Mouse secreted protein Zalpa37 degenerate coding sequence.
PN WO200138505-A2.
PD 31-MAY-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 34.0%; Score 789; DB 4; Length 1569;
Best Local Similarity 47.8%; Pred. No. 5.2e-224;
RESULT 52
ID ABA09537 standard; cDNA; 1898 BP.
DE Human PRO1780 homologue-encoding cDNA, SEQ ID NO:1313.

PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.

Query Match 30.5%; Score 708.2; DB 4; Length 1898;
Best Local Similarity 86.4%; Pred. No. 8e-200;

RESULT 53

ID AAF93971 standard; DNA; 770 BP.
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 405.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.

Query Match 25.7%; Score 595.2; DB 5; Length 770;
Best Local Similarity 93.4%; Pred. No. 2.4e-166;

RESULT 54

ID ADB62657 standard; cDNA; 1842 BP.
DE Human cDNA encoding clone KIDNE20186170.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 25.6%; Score 593.4; DB 10; Length 1842;
Best Local Similarity 85.6%; Pred. No. 1.5e-165;

RESULT 55

ID ADQ64368 standard; cDNA; 5002 BP.
DE Novel human cDNA sequence #1529.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 24.8%; Score 575.4; DB 12; Length 5002;
Best Local Similarity 85.3%; Pred. No. 6.9e-160;

RESULT 56

ID AAF94120 standard; DNA; 594 BP.
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 554.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.

Query Match 23.2%; Score 538.4; DB 5; Length 594;
Best Local Similarity 98.5%; Pred. No. 1.9e-149;

RESULT 57

ID AAS81804 standard; cDNA; 2220 BP.
DE DNA encoding novel human diagnostic protein #17608.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 21.0%; Score 487.6; DB 5; Length 2220;
Best Local Similarity 93.7%; Pred. No. 6.7e-134;

RESULT 58

ID ADN39359 standard; cDNA; 923 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:B43.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 19.0%; Score 441; DB 11; Length 923;
Best Local Similarity 100.0%; Pred. No. 3.1e-120;

RESULT 59

ID ABK90832 standard; DNA; 42999 BP.
DE Genomic DNA encoding drug metabolising enzyme.

PN US2002082194-A1.
 PD 27-JUN-2002.
 PA (GUEG/) GUEGLER K.
 PA (WEBS/) WEBSTER M.
 PA (YANC/) YAN C.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 Query Match 18.7%; Score 433.6; DB 6; Length 42999;
 Best Local Similarity 88.1%; Pred. No. 6.4e-117;
 RESULT 60
 ID AAS81803 standard; cDNA; 659 BP.
 DE DNA encoding novel human diagnostic protein #17607.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 17.2%; Score 399.6; DB 5; Length 659;
 Best Local Similarity 92.5%; Pred. No. 5.7e-108;
 RESULT 61
 ID AAS41046 standard; cDNA; 923 BP.
 DE cDNA encoding novel human enzyme polypeptide #262.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 13.8%; Score 319.6; DB 4; Length 923;
 Best Local Similarity 84.8%; Pred. No. 5.5e-84;
 RESULT 62
 ID AAS41586 standard; cDNA; 981 BP.
 DE cDNA encoding novel human enzyme polypeptide #802.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 13.8%; Score 319.4; DB 4; Length 981;
 Best Local Similarity 85.4%; Pred. No. 6.6e-84;
 RESULT 63
 ID AAL01667 standard; cDNA; 981 BP.
 DE Human reproductive system related antigen cDNA SEQ ID NO: 1668.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 13.8%; Score 319.4; DB 4; Length 981;
 Best Local Similarity 85.4%; Pred. No. 6.6e-84;
 RESULT 64
 ID ADQ57767 standard; DNA; 582 BP.
 DE Novel canine microarray-related DNA sequence SeqID9069.
 PN WO2004063324-A2.
 PD 29-JUL-2004.
 PA (GENE-) GENE LOGIC INC.
 PA (PFIZ) PFIZER PROD INC.
 Query Match 13.6%; Score 314.8; DB 13; Length 582;
 Best Local Similarity 81.8%; Pred. No. 1.1e-82;
 RESULT 65
 ID AAL05664 standard; DNA; 5973 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 8352.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 10.3%; Score 239.2; DB 4; Length 5973;

Best Local Similarity 86.0%; Pred. No. 2e-59;

RESULT 66

ID AAK11854 standard; DNA; 507 BP.

DE Human brain expressed single exon probe SEQ ID NO: 11845.

PN WO200157275-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 10.3%; Score 238.8; DB 4; Length 507;

Best Local Similarity 86.3%; Pred. No. 5e-60;

RESULT 67

ID AAL05663 standard; DNA; 2751 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 8351.

PN WO200155320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 10.3%; Score 238.8; DB 4; Length 2751;

Best Local Similarity 86.3%; Pred. No. 1.5e-59;

RESULT 68

ID AAL05665 standard; DNA; 5974 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 8353.

PN WO200155320-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 10.3%; Score 238.8; DB 4; Length 5974;

Best Local Similarity 86.3%; Pred. No. 2.6e-59;

RESULT 69

ID AAS84831 standard; cDNA; 1242 BP.

DE DNA encoding novel human diagnostic protein #20635.

PN WO200175067-A2.

PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.

Query Match 9.7%; Score 224; DB 5; Length 1242;

Best Local Similarity 100.0%; Pred. No. 2.4e-55;

RESULT 70

ID AAS82074 standard; cDNA; 1242 BP.

DE DNA encoding novel human diagnostic protein #17878.

PN WO200175067-A2.

PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.

Query Match 9.7%; Score 224; DB 5; Length 1242;

Best Local Similarity 100.0%; Pred. No. 2.4e-55;

RESULT 71

ID AAK24438 standard; DNA; 277 BP.

DE Human brain expressed single exon probe SEQ ID NO: 24429.

PN WO200157275-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 9.5%; Score 220; DB 4; Length 277;

Best Local Similarity 87.3%; Pred. No. 1.4e-54;

RESULT 72

ID ABI99695 standard; cDNA; 2308 BP.

DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:738.

PN WO200188188-A2.

PD 22-NOV-2001.

PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

Query Match 7.1%; Score 164; DB 6; Length 2308;

Best Local Similarity 47.5%; Pred. No. 3e-37;

RESULT 73

ID ACN45084 standard; DNA; 49753 BP.

DE Mouse genomic sequence mCG7831.

PN WO2003073826-A2.

PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.

Query Match 7.0%; Score 162.6; DB 11; Length 49753;

Best Local Similarity 72.7%; Pred. No. 6e-36;

RESULT 74

ID ADB59021 standard; DNA; 1716 BP.

DE Toxicity-related gene, SEQ ID 4047.

PN WO2003064624-A2.

PD 07-AUG-2003.

PA (GENE-) GENE LOGIC INC.

Query Match 6.4%; Score 148; DB 10; Length 1716;

Best Local Similarity 51.9%; Pred. No. 1.5e-32;

RESULT 75

ID ADB53779 standard; DNA; 1716 BP.

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4321.

PN WO2003065993-A2.

PD 14-AUG-2003.

PA (GENE-) GENE LOGIC INC.

Query Match 6.4%; Score 148; DB 10; Length 1716;

Best Local Similarity 51.9%; Pred. No. 1.5e-32;

RESULT 76

ID ADP73008 standard; DNA; 1716 BP.

DE Renal toxin progression gene marker #1597.

PN WO2004048598-A2.

PD 10-JUN-2004.

PA (GENE-) GENE LOGIC INC.

Query Match 6.4%; Score 148; DB 12; Length 1716;

Best Local Similarity 51.9%; Pred. No. 1.5e-32;

RESULT 77

ID ADP72663 standard; DNA; 1819 BP.

DE Renal toxin progression gene marker #1252.

PN WO2004048598-A2.

PD 10-JUN-2004.

PA (GENE-) GENE LOGIC INC.

Query Match 6.4%; Score 148; DB 12; Length 1819;

Best Local Similarity 51.9%; Pred. No. 1.5e-32;

RESULT 78

ID ABK63496 standard; cDNA; 1961 BP.

DE Rat sequence differentially expressed in response to a hepatotoxin #1403.

PN WO200210453-A2.

PD 07-FEB-2002.

PA (GENE-) GENE LOGIC INC.

Query Match 6.3%; Score 145.2; DB 6; Length 1961;

Best Local Similarity 49.4%; Pred. No. 1.1e-31;

RESULT 79

ID ADB57963 standard; DNA; 1961 BP.

DE Toxicity-related gene, SEQ ID 2989.

PN WO2003064624-A2.

PD 07-AUG-2003.

PA (GENE-) GENE LOGIC INC.

Query Match 6.3%; Score 145.2; DB 10; Length 1961;

Best Local Similarity 49.4%; Pred. No. 1.1e-31;

RESULT 80

ID ABZ58827 standard; cDNA; 1584 BP.
 DE Human 32624 polypeptide coding sequence.
 PN WO200226834-A2.
 PD 04-APR-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 6.2%; Score 144.2; DB 6; Length 1584;
 Best Local Similarity 48.4%; Pred. No. 1.9e-31;
 RESULT 81
 ID ABZ58826 standard; cDNA; 2996 BP.
 DE Human 32624 polypeptide encoding cDNA.
 PN WO200226834-A2.
 PD 04-APR-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 6.2%; Score 144.2; DB 6; Length 2996;
 Best Local Similarity 48.4%; Pred. No. 2.9e-31;
 RESULT 82
 ID AAD24666 standard; cDNA; 1636 BP.
 DE Human drug metabolising enzyme (DME)-1 cDNA.
 PN WO200179468-A2.
 PD 25-OCT-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 6.2%; Score 143.2; DB 6; Length 1636;
 Best Local Similarity 48.3%; Pred. No. 3.9e-31;
 RESULT 83
 ID ADA11047 standard; cDNA; 1636 BP.
 DE Human cDNA differentially expressed in colon cancer #117.
 PN US2002160382-A1.
 PD 31-OCT-2002.
 PA (LASE/) LASEK A W.
 PA (JONE/) JONES D A.
 Query Match 6.2%; Score 143.2; DB 9; Length 1636;
 Best Local Similarity 48.3%; Pred. No. 3.9e-31;
 RESULT 84
 ID ADS09871 standard; DNA; 2408 BP.
 DE Human therapeutic DNA - SEQ ID 108.
 PN WO2004080148-A2.
 PD 23-SEP-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 6.2%; Score 143.2; DB 13; Length 2408;
 Best Local Similarity 48.3%; Pred. No. 5e-31;
 RESULT 85
 ID ABK12422 standard; cDNA; 2759 BP.
 DE cDNA encoding human drug-metabolising enzyme.
 PN WO200218554-A2.
 PD 07-MAR-2002.
 PA (APPL-) APPLERA CORP.
 Query Match 6.2%; Score 143.2; DB 6; Length 2759;
 Best Local Similarity 48.3%; Pred. No. 5.5e-31;
 RESULT 86
 ID ADA10915 standard; cDNA; 2966 BP.
 DE Human cDNA differentially expressed in colon cancer #22.
 PN US2002160382-A1.
 PD 31-OCT-2002.
 PA (LASE/) LASEK A W.
 PA (JONE/) JONES D A.
 Query Match 6.2%; Score 143.2; DB 9; Length 2966;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 87

ID ADL12512 standard; cDNA; 2966 BP.
DE Human steroid-induced C3A liver cell cDNA #241.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.2%; Score 143.2; DB 12; Length 2966;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 88

ID AAS46185 standard; cDNA; 2974 BP.
DE Human DNA encoding PRO polypeptide sequence #261.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 4; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 89

ID ACA89635 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 90

ID ACA73645 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 91

ID ACA05960 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 92

ID ACA66794 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO protein #261.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 93

ID ACF20369 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 94

ID ACF19755 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003040064-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 95

ID ACD22043 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003027267-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 96

ID ACF13208 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036160-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 97

ID ACD25311 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003044925-A1.

PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 98

ID ACF00360 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003054474-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 99

ID ACA72417 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003032114-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 100

ID ACD04941 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003032101-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 101

ID ACD18402 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036124-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 102

ID ACD08409 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003040054-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 103

ID ACA88843 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036133-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 104

ID ACA70285 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036134-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 105

ID ACD12507 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003022294-A1.

PD 30-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 106

ID ACC74422 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027275-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 107

ID ACD16050 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003027324-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 108

ID ACD25618 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036118-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 109

ID ACD18095 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036123-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 110

ID ACC88382 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036148-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 111

ID ACD21736 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003040060-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 112

ID ACD18803 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003044916-A1.

PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 113

ID ABX98413 standard; cDNA; 2974 BP.

DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 521.

PN US2003036156-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 114

ID ACD14164 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003032117-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 115

ID ACD09944 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036128-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 116

ID ACC88689 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027266-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 117

ID ACD21429 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003054483-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 118

ID ABX75801 standard; cDNA; 2974 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO6239.

PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 119
ID ABX98004 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 120
ID ACA97480 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 121
ID ACA57943 standard; cDNA; 2974 BP.
DE Human PRO6239 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 122
ID ACD14471 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 123
ID ACC91254 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 124
ID ACC88996 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 125
ID ACD07193 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 126
ID ACA67644 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003017542-A1.

PD 23-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 127

ID ACC81699 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003032137-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 128

ID ACC89303 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027269-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 129

ID ACC86659 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027268-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 130

ID ACC89917 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027274-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 131

ID ACC93096 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003032135-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 132

ID ACA72724 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003022295-A1.

PD 30-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 133

ID ACA89242 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003022297-A1.

PD 30-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 134

ID ACA69978 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003032105-A1.
PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 135

ID ACA97121 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 136

ID ACA91117 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 137

ID ACA70899 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003032111-A1.
PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 138

ID ACA95409 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 139

ID ACC86352 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027263-A1.
PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 140

ID ACC90224 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027271-A1.
PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 141

ID ACD12832 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003036125-A1.
PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 142

ID ACF20062 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040068-A1.
PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 143

ID ABX77006 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003027280-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 144

ID ACA73338 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003022300-A1.

PD 30-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 145

ID ACA68881 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036136-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 146

ID ACA74725 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003036138-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 147

ID ACA70592 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003032109-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 148

ID ACD14778 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003040066-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 149

ID ACA68450 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003032104-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 150

ID ABX98915 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036157-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 151

ID ACC81392 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003032120-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 152

ID ACA95716 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036155-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 153

ID ACD04634 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003022296-A1.

PD 30-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 154

ID ACC88075 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027281-A1.

PD 06-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 155

ID ACF12737 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003040058-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 156

ID ACA96452 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003017540-A1.

PD 23-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 157

ID ACA65226 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003032106-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 158

ID ACA73952 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003032129-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 159

ID ACA74364 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003032131-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 160

ID ACA96759 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003032103-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 161

ID ACD10865 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003032107-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 162

ID ACC91561 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003032139-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 163

ID ACD02896 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003022301-A1.

PD 30-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 164

ID ACC87461 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036165-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 165

ID ACC86045 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027262-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 166

ID ACA65533 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003032110-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 167

ID ACA94350 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036142-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 168

ID ACA98094 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003036145-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 169

ID ACA91596 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036154-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 170

ID ACA90810 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003036153-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 171

ID ACD16357 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003044931-A1.

PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 172

ID ACD17518 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036150-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 173

ID ACC92175 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003040069-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 174

ID ACA75032 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003022293-A1.

PD 30-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 175

ID ACA91903 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003032128-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 176

ID ACA71547 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003032116-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 177

ID ACC90947 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003032122-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 178

ID ACA65957 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO protein #261.

PN US2003036139-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 179

ID ACA95102 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003017541-A1.

PD 23-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 180

ID ACD16664 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003017543-A1.

PD 23-JAN-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 181

ID ACD15743 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036152-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 182

ID ABX16846 standard; cDNA; 2974 BP.

DE Human cDNA encoding secreted/transmembrane protein #261.

PN US2002127584-A1.

PD 12-SEP-2002.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 8; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 183

ID ACA97787 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003032115-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 184

ID ACA99236 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003032140-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 185

ID ACC91868 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003040076-A1.

PD 27-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 186

ID ACD11279 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003008352-A1.

PD 09-JAN-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 187

ID ACD15129 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003044922-A1.

PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 188

ID ACD11893 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003032118-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 189

ID ACC96022 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036135-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 190

ID ACF16585 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003054455-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 191
 ID ACF02703 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049741-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 192
 ID ACF03010 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049743-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 193
 ID ACF21597 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049769-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 194
 ID ACF10281 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068743-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 195
 ID ACF78174 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054479-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 196
 ID ACD46879 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068685-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 197
 ID ACD49642 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068725-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 198
ID ACF28409 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 199
ID ACD89099 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 200
ID ACD84494 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 201
ID ACD99268 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 202
ID ADA78273 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 203
ID ACF49010 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 204
ID ACD09330 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 205
 ID ACF12123 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003040075-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 206
 ID ACF41357 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054459-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 207
 ID ACF15971 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003044930-A1.
 PD 06-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 208
 ID ACF16278 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003040071-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 209
 ID ACD32105 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003054471-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 210
 ID ACF18913 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064452-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 211
 ID ACF09360 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068705-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 212
 ID ACF78481 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 213

ID ACF52080 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064440-A1.
PD 03-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 214

ID ACF26567 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 215

ID ACF24360 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 216

ID ACF63671 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 217

ID ACF50545 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 218

ID ACH08016 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 219

ID ACF13822 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064462-A1.

PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 220
 ID ACD41748 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003065159-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 221
 ID ACF32161 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064447-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 222
 ID ACF23439 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003073184-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 223
 ID ACF40129 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064463-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 224
 ID ACD45651 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003064451-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 225
 ID ACF53308 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068721-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 226
 ID ACF27488 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068699-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 227

ID ACF45326 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003068707-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 228

ID ACF29944 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003073175-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 229

ID ACD90020 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003068695-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 230

ID ACD84801 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003068703-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 231

ID ACD98961 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003068732-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 232

ID ACF77253 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521....

PN US2003082717-A1.

PD 01-MAY-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 233

ID ACF76946 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003104548-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 234
 ID ACF49931 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003104542-A1.
 PD 05-JUN-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 235
 ID ACF50238 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003104543-A1.
 PD 05-JUN-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 236
 ID ACD09637 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003036127-A1.
 PD 20-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 237
 ID ACD08716 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003040061-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 238
 ID ACF12430 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003036130-A1.
 PD 20-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 239
 ID ACC94938 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054468-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 240
 ID ACD22657 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003054470-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 241
 ID ACF15357 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003044917-A1.
 PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 242
 ID ACC97452 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003044929-A1.
 PD 06-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 243
 ID ACC92482 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003059880-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 244
 ID ACF14129 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064465-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 245
 ID ACF14436 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054478-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 246
 ID ACF09667 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068718-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 247
 ID ACD45958 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003064454-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 248
 ID ACD48107 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003064461-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 249

ID ACD67838 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 250

ID ACF25646 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 251

ID ACF29330 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 252

ID ACD85108 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 253

ID ACD84187 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 254

ID ACD88178 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 255

ID ACF30865 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 256

ID ACF32468 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003104555-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 257
 ID ACH12128 standard; cDNA; 2974 BP.
 DE cDNA encoding human PRO polypeptide #261.
 PN US2003049768-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 258
 ID ACH12435 standard; cDNA; 2974 BP.
 DE cDNA encoding human PRO polypeptide #261.
 PN US2003049771-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 259
 ID ACD40827 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003032134-A1.
 PD 13-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 260
 ID ACF18299 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054481-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 261
 ID ACF08746 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049778-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 262
 ID ACF31547 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049782-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 263
 ID ACF52387 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 264
ID ACD50256 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 265
ID ACF38959 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 266
ID ACF26874 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 267
ID ACF24974 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 268
ID ACF46554 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 269
ID ACF28102 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 270
ID ACD89406 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068684-A1.

PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 271
 ID ACF63978 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003073179-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 272
 ID ACF60618 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003087374-A1.
 PD 08-MAY-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 273
 ID ACH12742 standard; cDNA; 2974 BP.
 DE cDNA encoding human PRO polypeptide #261.
 PN US2003049773-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 274
 ID ACH10165 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049777-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 275
 ID ACD04020 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003040055-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 276
 ID ACD10558 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003036164-A1.
 PD 20-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 277
 ID ACF42585 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054480-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 278

ID ACF18606 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 279

ID ACF02396 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 280

ID ACF21904 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 281

ID ACF10588 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073169-A1.
PD 17-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 282

ID ACF34040 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 283

ID ACF45002 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 284

ID ACD90634 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 285

ID ACD91247 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049751-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 286
 ID ACF30558 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003067478-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 287
 ID ACD87257 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068773-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 288
 ID ACF60311 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003073185-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 289
 ID ACF46861 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003087373-A1.
 PD 08-MAY-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 290
 ID ACF75718 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003096353-A1.
 PD 22-MAY-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 291
 ID ADA80065 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003073173-A1.
 PD 17-APR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 292
 ID ACF17378 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054458-A1.
 PD 20-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 293
 ID ACF23132 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003059886-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 294
 ID ACF08132 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049758-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 295
 ID ACF08439 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049772-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 296
 ID ACF40743 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064448-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 297
 ID ACF53922 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064456-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 298
 ID ACD47186 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068693-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 299
 ID ACF48089 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068735-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 300

ID ACF47475 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 301

ID ACF46247 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 302

ID ACD86336 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 303

ID ACF52694 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003082715-A1.
PD 01-MAY-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 304

ID ACF53001 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003082716-A1.
PD 01-MAY-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 305

ID ACF64994 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 306

ID ACF76639 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 307

ID ACF61539 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003096359-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 308
 ID ACF61846 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003100061-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 309
 ID ACD30877 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003032125-A1.
 PD 13-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 310
 ID ACD31798 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003054454-A1.
 PD 20-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 311
 ID ACD32719 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003054477-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 312
 ID ACF17685 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054460-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 313
 ID ACF07518 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049753-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 314
 ID ACF20676 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049763-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 315

ID ACF21290 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073172-A1.
PD 17-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 316

ID ACF20983 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073172-A1.
PD 17-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 317

ID ACD47800 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068700-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 318

ID ACF47782 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068736-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 319

ID ACF53615 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068679-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 320

ID ACD86950 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068767-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 321

ID ACH05198 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003073182-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 322

ID ACF44695 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 323

ID ADA81792 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 324

ID ACD22350 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003027276-A1.
PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 325

ID ACD24697 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003044920-A1.
PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 326

ID ACD39900 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003027265-A1.
PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 327

ID ACD40207 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 328

ID ACF13515 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 329

ID ACF03317 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049744-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 330

ID ACF78788 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003049783-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 331

ID ACF11509 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003073171-A1.

PD 17-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 332

ID ACF50852 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003032121-A1.

PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 333

ID ACF34347 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003064458-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 334

ID ACD46572 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003064460-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 335

ID ACD48414 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003064464-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 336

ID ACF27795 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003068702-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 337

ID ACF24667 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 338

ID ACD85722 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 339

ID ACD90327 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 340

ID ACD83880 standard; cDNA; 2974 BP.
DE Human PRO polynucleotide #261.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 341

ID ACF49317 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104540-A1.
PD 05-JUN-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 342

ID ACH07402 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 343

ID ACH07709 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 344

ID ACH08323 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 345

ID ACH11514 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 346

ID ACH11821 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 347

ID ACH10472 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 348

ID ACF01475 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040059-A1.
PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 349

ID ACF41050 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 350

ID ACD24390 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003044918-A1.
PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 351

ID ACD31491 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003032132-A1.
PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 352
 ID ACF17992 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003054462-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 353
 ID ACF32775 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064445-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 354
 ID ACF40436 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064449-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 355
 ID ACF48396 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064441-A1.
 PD 03-APR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 356
 ID ACF38345 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068696-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 357
 ID ACF25281 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068712-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 358
 ID ACF27181 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068730-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 359

ID ACF29637 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073174-A1.
PD 17-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 360

ID ACD87871 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 361

ID ACF76332 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 362

ID ACF49624 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104541-A1.
PD 05-JUN-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 363

ID ACF44081 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 364

ID ACH06426 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 365

ID ACH06733 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 366

ID ADA83590 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 367

ID ACC92789 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003032133-A1.
PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 368

ID ACC93403 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003032136-A1.
PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 369

ID ACF19448 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003036129-A1.
PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 370

ID ACD13139 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003040053-A1.
PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 371

ID ACF06597 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040057-A1.
PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 372

ID ACC94631 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054467-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 373

ID ACC98059 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003044932-A1.
PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 374

ID ACC94324 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027270-A1.
PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 375

ID ACF42278 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 376

ID ACD31184 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003032126-A1.
PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 377

ID ACD43213 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 378

ID ACD43520 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 379

ID ACF15050 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 380

ID ACF01782 standard; cDNA; 2974 BP..
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049738-A1.
PD 13-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 381

ID ACF31854 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 382
 ID ACD67531 standard; cDNA; 2974 BP.
 DE cDNA encoding human PRO polypeptide #261.
 PN US2003064453-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 383
 ID ACD48721 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003064466-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 384
 ID ACD49028 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003064468-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 385
 ID ACF51466 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068760-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 386
 ID ACF54229 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068769-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 387
 ID ACF25953 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003045700-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 388
 ID ACF39266 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068698-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 389
 ID ACF29023 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068759-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 390
 ID ACD90940 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049748-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 391
 ID ACD86643 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068765-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 392
 ID ACH05505 standard; cDNA; 2974 BP.
 DE cDNA encoding human PRO polypeptide #261.
 PN US2003049754-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 393
 ID ACF65301 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068688-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 394
 ID ADB20633 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003082767-A1.
 PD 01-MAY-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 395
 ID ACF43774 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003104552-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 396

ID ACH09244 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049774-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 397
 ID ACH09551 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049775-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 398
 ID ADA78885 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003073181-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 399
 ID ACF09974 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068720-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 400
 ID ACF51159 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068739-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 401
 ID ACF24053 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068763-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 402
 ID ACD88485 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068689-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 403
 ID ACH09858 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049776-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 404
 ID ACH10779 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049780-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 405
 ID ACD11586 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003036126-A1.
 PD 20-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 406
 ID ACC96636 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003044924-A1.
 PD 06-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 407
 ID ACC98666 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003044927-A1.
 PD 06-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 408
 ID ACF41971 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003040072-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 409
 ID ACF16892 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003040073-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 410
 ID ACD32412 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003054475-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 411

ID ACD30570 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003032124-A1.
PD 13-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 412

ID ACD41441 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 413

ID ACF07825 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 414

ID ACF31240 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 415

ID ACF77560 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 416

ID ACF11202 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073170-A1.
PD 17-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 417

ID ACF33082 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 418

ID ACF26260 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003068717-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 419

ID ACD83573 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003068728-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 420

ID ACF23746 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003068764-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 421

ID ACF43160 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003104550-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 422

ID ACF43467 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003104551-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 423

ID ACH06119 standard; cDNA; 2974 BP.

DE cDNA encoding human PRO polypeptide #261.

PN US2003049761-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 424

ID ACH08937 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003049757-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 425

ID ACC90531 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003027273-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 426

ID ACF10895 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036119-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 427

ID ACC93710 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036120-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 428

ID ACC96329 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003036161-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 429

ID ACD25004 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003044921-A1.

PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 430

ID ACF02089 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003049739-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 431

ID ACF22211 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003059882-A1.

PD 27-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 432

ID ACF22825 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003059884-A1.

PD 27-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 433

ID ACF09053 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068687-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 434
 ID ACF33389 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003073186-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 435
 ID ACF54843 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064443-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 436
 ID ACF48703 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003064444-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 437
 ID ACD47493 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068697-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 438
 ID ACD49335 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068710-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 439
 ID ACF38038 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068686-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 440
 ID ACF30251 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 441

ID ACD87564 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 442

ID ACF62153 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104538-A1.
PD 05-JUN-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 443

ID ACH11086 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 444

ID ACD10251 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003036158-A1.
PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 445

ID ACD16976 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003036151-A1.
PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 446

ID ACC99273 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003040067-A1.
PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 447

ID ACF00667 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054456-A1.
PD 20-MAR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 448

ID ACD41134 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 449

ID ACF14743 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 450

ID ACF22518 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 451

ID ACF79095 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 452

ID ACF11816 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 453

ID ACF51773 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 454

ID ACF33696 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 455

ID ACD49949 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068731-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 456
 ID ACF37731 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068683-A1.
 PD 10-APR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 457
 ID ACF28716 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003068754-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 458
 ID ACD88792 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003068681-A1.
 PD 10-APR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 459
 ID ACF75411 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003096351-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 460
 ID ACF61232 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003096358-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 461
 ID ACF44388 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003104556-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 462
 ID ACH08630 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003049756-A1.

PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 463
 ID ACC94017 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003036122-A1.
 PD 20-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 464
 ID ACD21122 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003036121-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 465
 ID ACF06904 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003040065-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 466
 ID ACD20815 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003044919-A1.
 PD 06-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 467
 ID ACD22964 standard; cDNA; 2974 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #261.
 PN US2003040077-A1.
 PD 27-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 468
 ID ACF41664 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003044928-A1.
 PD 06-MAR-2003.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 469
 ID ACF07211 standard; cDNA; 2974 BP.
 DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
 PN US2003049746-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 9; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 470
 ID ACF77867 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 471
ID ACD46265 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 472
ID ACF47168 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 473
ID ACF54536 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 474
ID ACF45940 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 475
ID ACF45633 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 476
ID ACF38652 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 477
ID ACD89713 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.